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using Induced Pluripotent Stem Cells

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## INTRODUCTION

Induced pluripotent stem (iPS) cells provide a valuable resource for identifying epigenetic changes that occur during cell differentiation because reprogramming reverses the process of cell specification through epigenetic modification, erasing tissue-specific DNA methylation and re-establishing the embryonic-like methylome.<sup>1,2</sup> iPS cells can then be re-differentiated into the desired cell type by appropriate inductive factors, and the epigenetic changes occurring throughout the differentiation process may be captured by temporal characterization of the epigenome as reported in embryonic stem cell (ESC) differentiation.<sup>3</sup> This process may be facilitated by the recently discovered epigenetic memory of iPS cells. Specifically, human iPS cells generated from hepatocytes (representative of endoderm), skin fibroblasts (mesoderm), and melanocytes (ectoderm) all retained a transcriptional memory of the original cells, which was partially explained by incomplete promoter DNA methylation.<sup>4</sup> In fact, both mouse and human iPS cells retain a residual DNA methylation pattern of the original somatic cells.<sup>5,6</sup> This epigenetic memory biases the differentiation potential of iPS cells toward lineages related to the cell of origin.<sup>6,7</sup>

Little is known about the epigenetic changes underlying prostate differentiation, partly because of the lack of suitable models. While cell cultures have been a valuable resource for discovery of epigenetic changes occurring during differentiation, these are largely limited to tumor cell lines or transformed derivatives that carry genetic and epigenetic artifacts of accommodation to cell culture.<sup>8,9</sup> Primary cultures are a more realistic model but have a limited life span.<sup>10</sup> If iPS cells could be generated from prostatic epithelial cells with defined factors, they would provide a tractable method for establishing immortal cultures of pluripotent cells from a single differentiated prostatic epithelial cell. Because the epigenetic changes that occurred during prostate differentiation will be erased in these iPS cells, these changes can be identified by comparing the epigenome of prostate epithelial cell-derived iPS cells and their differentiated progenies.

We hypothesize that primary prostate epithelial cells (E-PZ) can be reprogrammed to a pluripotent state by introducing a defined and limited set of transcription factors and by culturing under ESC conditions. Furthermore, these E-PZ-iPS cells can be re-differentiated back to E-PZ cells similar to those in the primary cancer by culturing under differentiation-inducing conditions. By comparing the epigenetic state of E-PZ-iPS cells and their differentiated progeny, alterations responsible for the prostate differentiation that are erased during the reprogramming can be identified on a genome-wide scale. Our specific aims are: 1) generating E-PZ-iPS cells using cultured primary epithelial cells by retroviral infection of E-PZ cells with viruses carrying Oct4, Sox2, Klf4, and c-Myc, 2) determining cellular and molecular characteristics of E-PZ-iPS including long-term proliferation potential, ESC marker expression, and DNA methylation status within the promoter region of pluripotency genes as well as the potential to differentiate into lineages representative of the three embryonic germ layers and the three cell types (basal epithelial, secretory epithelial, and neuroendocrine) that encompass the prostate epithelium as well as cancer cells that resemble the parental primary PCa cells, 3) dissecting epigenetic changes during E-PZ-iPS re-differentiation by mapping global DNA methylation during E-PZ-iPS re-differentiation and identifying genomic sites occupied by PcG proteins in E-PZ-iPS cells and their differentiated progeny.

## BODY

**Our first designated task was to generate E-PZ-iPS cells using E-PZ cells (months 1-12).** Our specific goals were to (a) Retroviral infect E-PZ cells with lentiviruses expressing Oct4, Sox2, Klf4, and c-Myc and (b) pick and expand iPS cell colonies. We accomplished (a) and (b) of this aim in the first year. Briefly, we reprogrammed two E-PZ cultures, E-PZ-1 and E-PZ-2, derived from normal peripheral zone prostatic tissues of two men aged 56- and 44-years old, respectively. We picked seven single colonies from reprogramming of E-PZ-1, and five from E-PZ-2.

**Our second designated task was to characterize and re-differentiate E-PZ-iPS-like cells (months 6-24).** We characterized two cell lines derived from each of E-PZ-1 and E-PZ-2 in detail, i.e., E-PZ-1-iPS-like-4 and -7 from E-PZ-1 and E-PZ-2-iPS-like-1 and -5 from E-PZ-2. Our specific goals were to: (a) determine cellular and molecular characteristics of E-PZ-iPS-like including ESC marker expression and DNA methylation status within the promoter region of pluripotency genes in reprogrammed cells with comparison of those characteristic of ESC and parental prostate epithelial cells, (b) assess the potential of E-PZ-iPS-like cells to differentiate into lineages representative of the three embryonic germ layers and the prostate epithelial cells in vitro, and (c) assess the potential of E-PZ-iPS-like cells to differentiate into lineages representative of the three embryonic germ layers and the prostate epithelial cells in vivo. We achieved all of the elements in this aim except the DNA methylation analysis of pluripotency genes for E-PZ-1-iPS-like-4 and -7 in the second year. This year, we determined DNA methylation levels of pluripotency genes and examined the karyotypes of E-PZ-1-iPS-like-4 and -7. Moreover, we characterized E-PZ-2-iPS-like-1 and -5 from E-PZ-2 in the same way as for E-PZ-1-iPS-like-4 and -7.

(a) We determined the methylation level of the promoter regions of Nanog and Oct4 in E-PZ-1 and E-PZ-1-iPS-like-4 and -7 cells by quantitative bisulfite pyrosequencing. Of the 6 CpG sites examined in the Nanog promoter, 3 showed demethylation in E-PZ-1-iPS-like cells compared to parent cells, while the other 3 didn't show significant changes in methylation (Fig. 1A). For the Oct4 promoter, 3 of 7 CpG sites showed

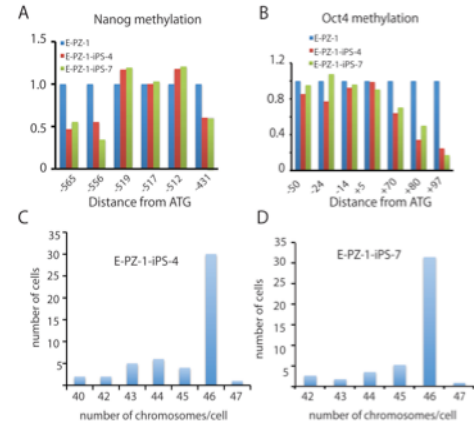


Fig. 1. Determination of methylation levels of Nanog and Oct4 and karyotype of E-PZ-1-iPS-like-4 and -7 cells. Methylation of Nanog (A) and Oct4 (B) promoters were determined by bisulfite pyrosequencing. The number of chromosomes in 100 E-PZ-1-iPS-4 (C) and -7 (D) cells were determined by metaphase chromosome counting.

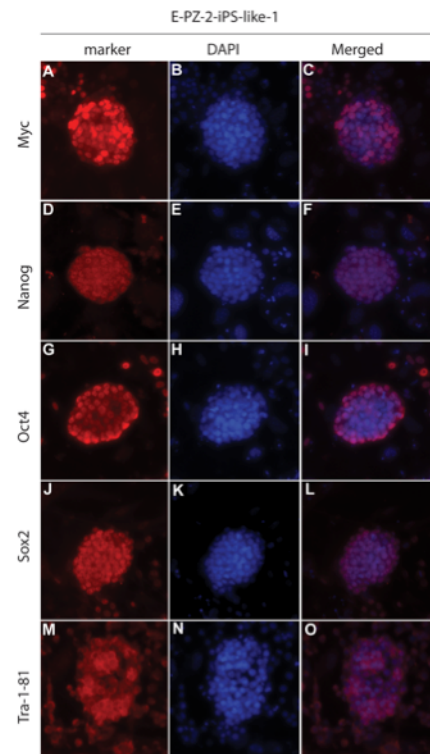


Fig. 2. Immunofluorescence detection of pluripotency gene expression in E-PZ-2-iPS-like-1 cells. E-PZ-2-iPS-like-1 cells showed strong nuclear staining of c-Myc (A), Nanog (D), Oct4 (G), Sox2 (J), and membrane staining of Tra-1-81 (M). (B), (E), (H), (K) and (N) are DAPI staining of the nuclei of the same cells in (A), (D), (G), (J), and (M), respectively. (C), (F), (I), (L), and (O) are merged images of (A) and (B), (D) and (E), (G) and (H), (J) and (K), (M) and (N), respectively.

demethylation while the other 4 did not (Fig. 1B). Chromosome spread counting demonstrated a normal karyotype, i.e. diploid, of E-PZ-1-iPS-1 and -7 cells (Fig. 1C-D). These results demonstrate epigenetic remodeling of the Oct4 and Nanog promoters in the E-PZ-iPS-like cells and are indicative of partial reprogramming.

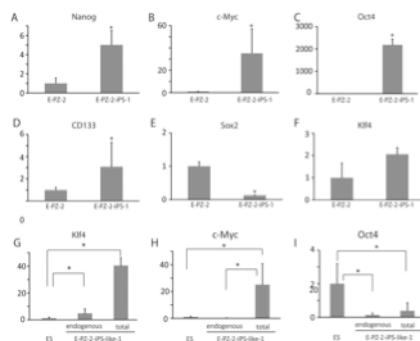


Fig. 3. Expression levels of pluripotent genes in E-PZ-2-iPS-like-1 cells. mRNA levels of Nanog (A), total c-Myc (B), total Oct4 (C), CD133 (D), total Sox2 (E), and total Klf4 (F) in E-PZ-2-iPS-like-1 cells were compared to parent E-PZ-2 cells. Total and endogenous Klf4 (G), total and endogenous c-Myc (H), and total and endogenous Oct4 (I) were measured by qRT-PCR and normalized against TBP. In (A)-(F), the Y-axis is the fold-level of gene expression in E-PZ-2-iPS-like cells compared to those in E-PZ-2 cells, which were set as 1. In (G)-(I), the Y-axis is the fold-level of gene expression in E-PZ-2-iPS-like cells compared to those in ES cells, which were set as 1. Asterisks indicate statistical significance by t-test.

We characterized the immunophenotype of E-PZ-2-iPS-like-1 and -7 cells by immunofluorescent staining of these cells with antibodies against TRA-1-81, SSEA-3, Nanog, Sox2, Oct4, and Myc as reported last year. As shown in Fig. 2, these cells gained pluripotent gene expression in E-PZ-2-iPS-like-1 cells typical of iPS cells. In addition, quantitative PCR demonstrated that in E-PZ-2-iPS-like-1 cells, expression levels of Nanog, total c-Myc, total Oct4, and CD133 were significantly increased compared to parental E-PZ-1 cells (Fig. 3). Similar to E-PZ-1-iPS-like-4 cells, Sox2 expression was decreased in E-PZ-2-iPS-like-1 cells. Expression levels of both Klf4 and c-Myc were significantly higher than that in H9 hES cells, while Oct4 expression was lower. Overall, our results indicate that the expression levels of pluripotency genes are increased although not identical to ESC.

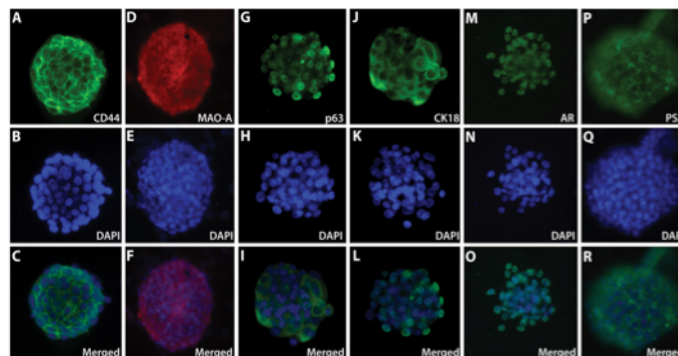


Fig. 4. In vitro differentiation of E-PZ-2-iPS-like-1 cells. E-PZ-2-iPS-like-1 cells cultured in E-PZ medium expressed basal prostatic epithelial cell markers including CD44 (A), MAO-A (D), and p63 (G). In addition, some spheres expressed CK18 (J) and AR (M) in the presence of R1881. When co-cultured with rat UGS, a subset of the spheres expressed PSA (P). (B), (E), (H), (K), (N) and (Q) are DAPI staining of the nuclei of the same cells in (A), (D), (G), (J), (M), and (P) respectively. (C), (F), (I), (L), (O), and (R) are merged images of (A) and (B), (D) and (E), (G) and (H), (J) and (K), (M) and (N), (P) and (Q), respectively.

**(b)** We determined whether E-PZ-iPS-like cells could be directed to differentiate into prostatic epithelial cells in vitro. Spheres derived from E-PZ-iPS-like cells and cultured in E-PZ medium expressed basal prostate epithelial cell markers including CD44 (Fig. 4A), MAO-A (Fig. 4D), and p63 (Fig. 4G), similar to the parental E-PZ cells. In addition, some spheres expressed CK18 (Fig. 4J), indicating a transit amplifying cell phenotype.

Unlike the parental E-PZ cells, which are negative for androgen receptor (AR), the spheres also expressed a low level of AR, which was upregulated

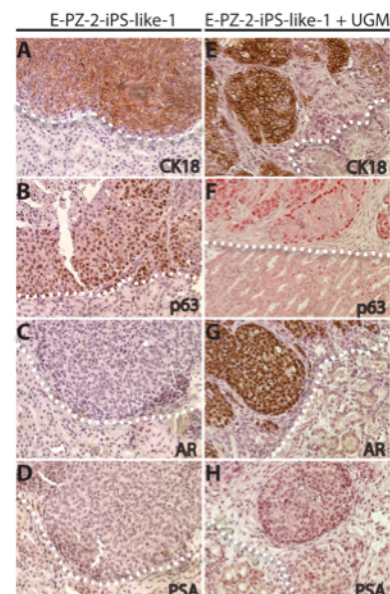


Fig. 5. In vivo differentiation of E-PZ-2-iPS-like-1 cells. E-PZ-2-iPS-like-1 cells injected under the renal capsule of immunodeficient mice expressed basal prostatic epithelial markers p63 (B) and transit amplifying epithelial cell marker CK18 (A), but not the secretory cell markers AR (C) or PSA (D). When combined with UGM, E-PZ-2-iPS-like-1 cells gave rise to cell clusters that uniformly expressed CK18 (E), and p63 but only at the edge (F). Although the cells were negative for PSA (H), they expressed AR in the nuclei (G). White dotted lines mark the boundary of grafts derived from E-PZ-2-iPS-like-1 cells and mouse kidney.

upon supplementation of R1881, a synthetic androgen, to the medium (Fig. 4M). Moreover, when co-cultured with rat urogenital sinus (UGS), which has been shown to induce prostatic differentiation,<sup>11</sup> a subset of the spheres derived from E-PZ-iPS-like cells expressed prostate-specific antigen (PSA) (Fig. 4P). These results suggest that E-PZ-iPS-like cells have the capacity to differentiate into prostatic epithelial cells.

(c) We determined the differentiation patterns of E-PZ-2-iPS-like-1 cells in vivo by subrenal capsule injection in immunodeficient mice. After eight weeks, tissue masses formed under the renal capsule with 100% frequency. Similar to E-PZ-1-iPS-like-4 cells, we did not observe teratoma-like histology in the tissue masses, instead, they expressed luminal epithelial cell marker CK18 (Fig. 5A), and basal prostate epithelial marker (Fig. 5B). They are negative for AR (Fig. 5C) and PSA (Fig. 5D). These results suggest that E-PZ-iPS-like cells retained the capability of differentiating into parental E-PZ-like cells in vivo.

We attempted to induce further differentiation of the E-PZ-iPS-like cells toward the prostate lineage by combining the cells with rat urogenital mesenchymal (UGM) cells, which have been shown to induce prostate differentiation previously. In the presence of UGM and androgen supplementation, different marker expression patterns were observed compared to that in the absence of UGM. Specifically, the basal prostate epithelial cell marker p63 was expressed by only the cells at the edge of the cell clusters (Fig. 5F) instead of all cells in a cluster (Fig. 5B). Moreover, although the cells were negative for PSA (Fig. 5H), they expressed CK18 (Fig. 5E) and AR in the nuclei (Fig. 5G), whereas no AR expression was observed in the absence of UGM (Fig. 5C). These results suggest that in the presence of UGM, E-PZ-iPS-like cells were induced toward a more complete prostate differentiation with cells displaying both basal and epithelial characteristics.

**Our third designated task was to identify epigenetic changes occurring during re-differentiation of E-PZ-iPS-like cells (months 24-36).** Our goal is to delineate the epigenetic changes occurring during the re-differentiation of E-PZ-iPS cells by capturing the epigenetic changes at different time points after induction of differentiation. Our specific goals are: (a) Mapping global DNA methylation during E-PZ-iPS re-differentiation; (b) Identifying genomic sites occupied by PcG proteins in E-PZ-iPS cells and their differentiated progeny. We have accomplished element (a) of this aim this year. We will complete (b) during the no-cost extension period that we have received for this award.

(a) We analyzed temporal methylation changes occurring during the induction of secretory prostatic differentiation of E-PZ-1-iPS-like-4 cells using DNA methylation profiling. DNA methylation levels of >485,000 sites were measured in spheres generated from E-PZ-1-iPS-like-4 cells cultured either in iPS cell medium as control, or in Complete PFMR-4A medium with 10 nM R1881 to induce AR expression for 1 or 3 days. In addition, spheres cultured in Complete PFMR-4A medium with 10 nM R1881 in the presence of UGS to induce PSA expression were harvested at 1, 3, or 5 days to capture methylation changes during mature secretory cell differentiation. In all, 5 pairs of samples were compared in the study, i.e., AR day 1 vs. control, AR day 3 vs. control, PSA day 1 vs. control, PSA day 3 vs. control, and PSA day 5 vs. control. Changes in methylation levels were examined in two ways. First, fold-change was calculated for each pair of samples as methylation level in induced cells divided by that in corresponding control cells. We focused on genes whose methylation levels increased or decreased by at least

50% in induced cells compare to corresponding control cells in at least 3 pairs of samples. Second, student's t-test was performed between the 5 control and 5 induced cells as two groups. Only genes with significant differential methylation levels in control vs. induced groups were selected. After filtering data with these two criteria, we identified 398 genes and 250 genes that were consistently and significantly hyper- or hypo-methylated in induced cells compared to control, respectively (Appendix A). The fold-changes of these genes in induced vs. control cells are shown in Fig. 6A.

Ingenuity Pathways Analysis (IPA) was performed to identify biological functions enriched for the 398 or 250 genes. For example, the top biological function in which the 398 hypermethylated genes in induced cells were enriched is embryonic development with >60 specific processes (Appendix B). In particular, formation of prostatic bud was significantly affected ( $p=0.0138$ ) through increased methylation of BMP7 and Wnt5A. It has been shown that newborn rat prostate cultured with exogenous Wnt5a protein exhibited signs of delayed maturation and secretory cell differentiation,<sup>12</sup> suggesting that Wnt5a inhibits secretory differentiation. This is consistent with increased methylation of Wnt5a, which has been shown to silence Wnt5a expression,<sup>13, 14</sup> in the differentiation of E-PZ-iPS-like cells toward the prostatic secretory cell lineage.

We further compared methylation levels in cells cultured under AR induction conditions for 1 vs. 3 days, and PSA induction conditions for 1 vs. 5 days. Genes that showed >4-fold higher or lower methylation levels were selected for further analysis. IPA analysis identified key canonical pathways and upstream regulators that have been shown to play important roles in prostatic differentiation (Fig. 6B and Appendix C). As expected, genes functioning in human ESC pluripotency were significantly hypermethylated in AR- and PSA- induced cells at later time points compared to day 1 (Fig. 6B). Similarly, PTEN pathway components were significantly hypermethylated in both differentiation processes, consistent with the recent finding that conditional ablation of PTEN in prostate basal cells promotes basal-to-luminal differentiation in mice.<sup>15</sup> Moreover, Nkx3.1, the earliest known marker of prostate epithelium during embryogenesis, was identified as a significant upstream regulator of genes that were demethylated in cells cultured under PSA-inducing conditions for 5 days compared to those for only 1 day (Appendix C), consistent with the finding that Nkx3.1 knock-out resulted in defects in prostate ductal morphogenesis and secretory protein production.<sup>16</sup> These results demonstrated that DNA methylation profiling using E-PZ-iPS-like cells undergoing differentiation captured epigenetic changes in key genes and pathways that are known to play important roles in prostatic differentiation. The epigenetic changes identified using E-PZ-iPS-like cells as a model may serve as a valuable resource for dissecting the mechanisms of prostatic differentiation.

## KEY RESEARCH ACCOMPLISHMENTS

- Determined cellular and molecular characteristics of E-PZ-iPS-like cells including ESC marker expression and their potential to differentiate into lineages representative of the prostatic epithelial cells in vitro.
- Assessed the potential of E-PZ-iPS-like cells to differentiate into lineages representative of the prostate epithelial cells in vivo.
- Identified temporal DNA methylation changes during re-differentiation of E-PZ-iPS-like cells into prostatic epithelial cells in vitro.



## REPORTABLE OUTCOMES

Zhao, H., Sun, N., Young, S.R., Nolley, R., Santos, J., Wu, J.C. and Peehl, D.M. Induced pluripotency of human prostatic epithelial cells. Submitted to PLoS One

## CONCLUSIONS

We have demonstrated that iPS-like cells derived from prostatic epithelial cells are pluripotent and capable of prostatic differentiation. In addition, DNA methylation profiling identified epigenetic changes in key pathways and genes involved in prostatic differentiation as E-PZ-iPS-like cells converted to differentiated AR- and PSA-expressing cells. Therefore, E-PZ-iPS-like cells provide a novel model for investigating epigenetic changes involved in prostate cell lineage specification.

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## APPENDICES

A. Genes that are hyper- or hypo-methylated across 5 pairs of samples at different time points of AR or PSA induction.

B. IPA analysis identified embryonic development as the top biological function in which hypermethylated genes were enriched during AR and PSA induction.

C. Canonical pathways and upstream regulators identified by IPA.

# **Appendix A Genes that are hyper- or hypo-methylated across 5 pairs of samples at different time points of AR or PSA induction.**

hypermethylated

gene symbol	log 2 ratio AR Day 1	log 2 ratio AR Day 3	log 2 ratio PSA Day 1	log 2 ratio PSA Day 3	log 2 ratio PSA Day 5
A1BG	0.629774111	0.391676339	0.901534263	-0.061645173	1.573084658
ABCF1;ABCF1	0.441910026	1.607638442	0.697256967	0.853673931	2.016105338
ABCF2;ABCF2	1.351008644	0.623879234	0.393981974	-0.036024306	1.279169591
ABHD2;ABHD2	0.650193078	1.01135336	0.495834004	0.714191483	0.7540348
ADAMTS19	1.069984639	0.897823753	-0.087017155	-0.061176114	0.833301203
ADAMTSL4;ADAMT	0.760491627	1.125022627	0.986038029	-0.230857013	0.195900074
ADH1C	0.940539427	0.193482532	-0.240232053	0.614482914	0.680933553
ADM	-0.184143886	2.171811245	0.797426097	0.480901446	0.706097477
AGAP1;AGAP1	0.582231596	0.768204989	-0.273907501	0.674679087	0.688591884
AHCYL1;AHCYL1	0.255107217	1.137520529	1.699337095	0.935863569	0.427279826
ALG5;ALG5	0.122941075	1.330622233	1.280945217	0.76250721	1.493534476
ALOXE3;ALOXE3	-0.503511113	0.914830356	1.026224602	1.033272788	1.070534636
AMD1;AMD1	1.063438311	0.996989636	0.517158545	0.423870266	1.340096262
AMN	0.329509981	-0.356645788	1.826284269	1.03222436	1.269256571
AMOT	0.771590238	2.915150478	1.854053488	0.117535656	-0.127766683
AMZ1	0.4111332	2.11436932	0.355735432	2.24124369	0.697954309
ANLN;KIAA0895	1.103817005	2.084595296	0.068478199	0.807995224	1.540762116
ANTXR1;ANTXR1;	0.446425502	1.101864089	-0.048852038	1.259478732	0.954405929
AP3B1	1.34161304	1.202936526	-0.713944033	1.164910779	1.067880004
APLP2;APLP2;APLP	3.535661917	3.747868456	2.309853772	-0.159175721	1.003935949
AQR	1.931903438	1.335579567	0.928533958	-0.072180338	1.340508252
ARG2	1.128218828	0.073402798	1.152788042	0.648295432	0.719873918
ARHGAP10	0.725013191	1.140397803	0.282891635	0.58832199	0.510778831
ARHGAP12	0.988606708	0.951784979	1.106468386	0.9627748	0.401660702
ARHGAP29;ARHGAP	0.943907213	1.052821824	0.920385094	1.343426712	0.833028286
ARHGEF7;ARHGEF	1.571117835	2.35840851	1.372354636	1.335147062	0.093996009
ARHGEF9;ARHGEF	0.712733955	0.080786681	0.342689238	0.948685869	1.625114142
ARID1B;ARID1B;A	0.238441362	0.78492675	0.261231078	0.630337956	0.759334063
ARMC8;ARMC8;AR	0.46349072	0.754841934	-0.020539802	0.599073058	0.636312616
ARVCF	0.511721027	0.886962688	0.727217982	0.900121675	0.069896816
ATF4;ATF4	0.736602499	0.741843671	0.193684563	0.725553496	0.535304268
ATG2A	0.026592712	1.846001244	1.148488313	0.135632504	1.223715155
ATG4C;ATG4C;ATC	0.340131058	3.607030098	1.748280547	1.359805337	0.127215402
AURKAIP1;AURKAIP	0.245868761	0.815952365	1.020417799	0.797723426	0.416039178
BAT2	2.410813447	0.686602639	1.484446421	1.142984301	1.826615214
BCL7C	0.40436054	0.826121699	0.416927507	1.481746489	0.702564959
BCYRN1;TAF1;TAF	1.461183869	0.219116885	1.18031824	0.447779393	1.172606125
BHLHE23	0.64655353	0.46318666	0.302763032	1.490749114	0.791641565
BMP7	0.819806814	0.584710395	-0.079125561	0.85874775	0.889133025
BNIP3	0.89099523	0.251545605	1.048006704	1.629478387	2.309277789
BTG2	0.38519336	1.404911104	1.756414964	0.872725073	2.909860623
BZW1	-0.130226178	0.161419933	1.577221458	1.535504196	2.026345756
C11orf60;C11orf60	0.179724084	0.786156023	0.094286763	1.083530442	0.806979096

C12orf75;C12orf7!	0.687558491	0.885801102	0.823160798	0.124961818	0.52879475
C14orf162	0.455934835	0.943970616	-0.0939444	1.480117466	1.227055159
C17orf96	-0.050769671	0.488539408	1.63576331	1.316121131	2.697132837
C19orf52;YIPF2;C	0.341716447	1.314950496	1.72117536	0.830935267	0.861680001
C1orf198;C1orf19!	0.581057232	0.891100584	1.378753665	-0.267664274	2.471193267
C1orf25;C1orf26;C	1.991695395	1.38527337	0.864357182	-0.23998862	1.440697455
C1orf63	1.897751442	-0.154699703	0.604637954	1.054245029	0.051314986
C1QTNF7	-0.056082423	0.740110741	0.239600642	1.251279316	1.454026754
C20orf108	0.803015773	0.205960309	0.3595893	0.920307611	0.97917919
C22orf9	0.977934393	0.195842003	0.821185314	0.173526754	0.738469214
C2orf74;C2orf74	0.415045453	0.871575467	0.675757401	-0.028967021	0.768144803
C6orf174	0.664536865	1.087760792	0.677250909	1.015178109	0.044124391
C7orf28B	1.517256002	1.333075119	-0.07383416	1.233899992	1.44757872
CABP1;CABP1;CAE	-0.0897432	0.834546618	0.69196712	0.682229368	0.331369918
CACNA1G;CACNA1	0.878202617	0.871476682	0.684358822	0.61155112	2.993594469
CADPS;CADPS;CA	-0.449222571	0.721176563	0.651605508	0.954936342	2.550957585
CASC5;CASC5	1.304480003	0.159187117	-0.048603642	0.813549554	0.808812823
CCDC14	-0.13708976	1.7120891	1.256809503	2.31858898	2.947903426
CCDC152	0.504396332	0.652266252	0.628742498	1.644248741	-0.15672912
CCDC46;CCDC46	0.559410461	-0.03583279	1.395650305	0.868826466	1.057378972
CCDC99;CCDC99	0.959703412	3.407855138	1.018368572	-0.597449746	0.625562475
CCND2	0.267559317	0.741185997	0.6547615	1.438617058	0.807242689
CCNT1	-0.41235085	0.924580403	0.926251831	1.521119696	1.716553875
CD37;CD37	-0.001096444	0.022382135	0.72743979	1.12553359	1.184017154
CD47;CD47;CD47	0.396480862	1.962834394	-0.260650997	1.28505847	1.738546787
CDH18;CDH18;CD	0.747481234	0.320490809	1.924904395	0.196062354	5.847145221
CEPT1;DRAM2;CEI	0.86037965	0.793990214	0.735312542	-0.042118694	1.275050909
CFL2;CFL2;CFL2;C	0.587197429	0.640320374	1.333883926	0.367119453	0.457229854
CHD9	0.772185999	0.130903568	1.459457356	1.23734013	0.38939093
CKAP2L;CKAP2L	1.142444229	1.052593592	-0.503827277	1.228500811	1.210660799
CLCN5;CLCN5;CLC	2.045222435	0.957268151	1.162047005	0.409392916	0.84184729
CNKS2;CNKS2;CN	0.901306127	0.219048161	1.074833878	1.709514051	2.048688368
CNP	0.016466063	1.674750116	1.287333172	1.138679893	0.250000583
COX18	-0.06862156	-0.317282965	0.931705408	0.914135613	0.735152593
CREG2	0.63208402	1.040579684	0.078765487	1.159967397	1.283112917
CRIP2	-0.079781528	1.651597819	0.246372199	0.971963949	2.462245971
CRISPLD1	0.194379587	1.48649455	0.259253429	1.321295898	0.986416325
CRMP1;CRMP1	0.530096301	0.868502026	0.046817329	0.593266206	0.7782214
CSNK1D;CSNK1D	0.134104159	3.525643973	0.934390497	-0.018446087	0.723327375
CTNNA2;CTNNA2;	-0.051986678	0.66957271	1.118592591	0.615777943	0.163666389
CTNNB1;CTNNB1;	0.771264011	1.219345205	-0.623871381	0.554966889	0.741340022
CYP20A1	0.927081109	0.918968425	0.296558628	0.020326303	0.954580983
DBN1;DBN1	0.158254292	0.723613037	1.134802703	0.345975973	1.163989428
DDX27	0.081740364	2.100946014	1.117583331	0.06286972	1.250292611
DDX28;DUS2L	0.87629332	1.953697072	0.616758193	0.951772303	1.510568691
DDX39	0.095130241	0.238113265	0.860027104	0.834959182	1.066620204
DDX60L	1.193438672	0.429996	-0.101146226	1.641648701	1.067960925
DEFB129	0.185548093	0.609415664	1.405857534	1.962654554	0.514729235
DHX15	0.41659738	1.582148166	0.596544473	1.073849658	0.93117062

DIMT1L	0.944719271	1.294449277	0.556431226	1.557248805	0.662828628
DKC1;DKC1	0.86127028	0.677728977	0.722915214	0.136883417	-0.001004735
DNTTIP2	0.868160048	3.350918627	1.006951034	-0.561332697	1.88480458
DPY19L3	0.630523427	1.031139501	0.38275048	0.919301175	1.498581562
DTNBP1;DTNBP1;I	1.037261988	0.627032532	0.087198367	0.244509124	0.666246213
DYNC1LI2	0.253176205	0.736824489	0.477983519	0.69728418	0.586259149
DYX1C1;DYX1C1;I	1.06485839	0.784211198	0.406634051	0.115117533	1.700794523
EDN1;EDN1;EDN1	0.549444517	0.54988731	0.627529532	1.276712478	2.050636243
EFNA4;EFNA4;EFN	0.455424862	1.070014288	1.312012074	0.227889384	0.952461762
EGFLAM;EGFLAM;I	-0.093836795	1.570323507	0.887434882	0.407056	3.78274351
ELMOD3;ELMOD3;	0.501701746	1.643623593	-0.247251365	0.605650363	1.738888758
ELMOD3;ELMOD3;	1.00238252	0.425859653	2.902478945	0.550725141	0.796569418
ELMOD3;ELMOD3;	0.600028428	0.902555684	0.329610636	1.265588847	0.361181352
ENOPH1;HNRPDL;	0.469113408	2.011702317	1.079121473	1.214638655	1.068374039
ENPP2;ENPP2;ENP	-0.28832833	0.442648047	0.800142258	1.301420963	0.915662274
ENTPD1;ENTPD1;E	0.788582256	0.619132622	-0.019346123	0.040151208	1.13629518
EPB41L5	0.499009723	0.782369417	0.135317368	0.767933599	0.836880912
ERGIC1;ERGIC1	0.184474861	0.821858588	2.764895702	3.231615835	4.326222287
ESRRG;ESRRG;ES	0.809085273	1.354214605	1.025128039	1.00865661	1.305389505
ESX1	1.120268631	0.80820098	-0.200380243	0.244115504	0.92126297
FAIM;FAIM;FAIM;F	0.688647928	0.754085183	-0.297228845	0.391029568	1.198190216
FAM123A;FAM123;	0.376924966	0.722829552	-0.115378201	1.127735091	1.007058148
FAM13A;FAM13A	0.239636436	1.505488125	0.206581797	1.459027049	0.627703221
FAM164C;FAM164C	0.25519933	0.738465269	1.521800887	-0.098751974	1.594634115
FAM180A	-0.26256452	0.617231708	0.941973465	0.363588187	1.282750556
FAM21A	0.878174956	0.439816641	1.975505255	0.098759381	2.301955828
FAM46C	0.063178386	1.535157866	0.922812348	1.095351501	2.525797606
FAM53C;FAM53C	0.392022667	0.652572056	0.248354607	1.723457781	0.849965134
FAM60A;FAM60A;F	0.766380284	0.988032307	0.68716588	0.553566297	0.227565082
FBXO27	1.788579443	0.700995455	1.184496916	0.097167975	1.200270173
FBXO4;FBXO4	0.482227357	0.739372094	0.180710717	1.092482318	0.74042302
FBXO8;KIAA1712;	1.024837392	2.138187689	0.125067154	-0.038910132	0.888833681
FGF14;FGF14	0.967922848	0.611529325	0.966949642	0.490051309	0.875490056
FIGNL1;FIGNL1	0.488912491	1.067769987	1.218849762	0.255006381	0.65979708
FLJ35220;LOC100	1.555553273	0.845427909	-0.262103831	1.222814291	0.259069123
FNDC7	0.652329252	1.12277667	0.60141773	0.062049916	0.372388274
FOXI1;FOXI1	1.174295793	-0.269280372	0.649358502	0.292332962	0.798919866
FOXJ3	1.281507015	1.325902229	1.598646741	-0.305639137	1.620375152
FOXO4;FOXO4	-0.42417517	1.860221804	1.187344494	2.291902677	3.017199501
FRAT2	0.973095982	0.69524549	3.276671465	0.464499464	0.787281512
FTH1	1.094726789	1.044005594	0.36566749	1.633169826	2.201740622
FTSJ3;PSMC5;FTS	0.921205341	1.515506555	-0.076747634	0.526514505	0.776922333
G6PD;G6PD;IKBK	1.546759411	0.790229019	1.170302314	0.251193618	0.421424132
GABRA2;GABRA2	0.769662496	0.795461224	-0.234745196	0.886288879	0.311142821
GALNTL4	1.123968183	-0.059986346	1.295907639	0.710143442	0.069991115
GCLC	1.03510873	0.939875334	1.253567255	1.230766126	1.767241992
GHR	0.88307624	0.759775941	0.533584133	2.660967746	1.524839825
GLUL;GLUL;GLUL;	2.45857458	2.014343499	0.418358182	2.032058977	-0.17780494
GMCL1	1.665375167	0.689826495	0.378404711	1.090734405	0.749085214

GPAM	0.748587727	-0.037438501	-0.155216525	1.214349163	0.774506535
GPC5	0.303050045	0.901455744	0.634849092	1.292651625	0.552009201
GPC5	-0.446400255	1.368125904	1.004645954	0.39560465	1.174075546
GRASP	-0.333244365	1.851072689	0.885515529	1.275924176	0.858236953
GRIA3;GRIA3	0.83646051	1.220660262	1.686507742	0.528382621	1.589202515
GRID1	0.903566644	0.594238792	0.277361361	1.693250974	0.799742822
GRP;GRP;GRP	0.35966803	0.72846377	0.582529255	0.708365871	0.940480785
GSTO2	1.382062294	0.026771656	0.29696916	1.350118814	2.608640751
GSTT1	1.848362381	2.028857629	0.544975777	2.82377459	0.306764085
GTF2H2C;GTF2H2C	0.666496927	1.137878702	1.30981668	-0.016398185	0.671419333
GTPBP10;GTPBP10	0.848176021	0.601217213	0.321430372	0.276941304	0.919013426
GTPBP8;GTPBP8	4.19947484	2.316447324	1.561849691	0.517457888	-0.653525581
H2AFV;H2AFV;H2AFV	0.766570828	0.92092472	0.308295398	0.16384702	0.950003799
H3F3B	2.802423806	2.345370969	2.054654897	-0.268486795	0.435403632
HCG22	0.170064493	1.240327939	1.460076194	1.482548368	1.012655524
HCG4	2.566135835	1.246172307	-0.221642174	0.93253783	2.217995194
HDAC10;HDAC10	2.05547826	1.07567123	0.236131295	0.438781675	0.638908479
HEATR7A;HEATR7A	0.399628771	0.574750119	0.872245829	1.167155117	2.715946566
HELZ	1.447517133	0.131220235	1.687710304	1.2354032	0.308296972
HERC4;HERC4	0.683237311	0.024359502	0.62322584	2.162903565	0.740360308
HHIP	0.575236775	2.556131216	0.330136598	1.322098322	0.638790229
HIRA;MRPL40	1.122966827	-0.214347326	0.730984105	2.103918622	0.468228556
HIST1H1C	0.852759195	0.264764275	0.61810244	0.240074092	1.412601547
HIST1H1D	1.267711257	0.851085873	0.84625871	0.900389682	0.43105719
HIST1H2BB;HIST1H2BB	1.127247138	0.894124713	1.153359102	3.365862128	0.063999342
HIVEP3;HIVEP3;HIVEP3	-0.075751471	2.137601528	1.375629963	1.019469611	0.924126278
HK1;HK1;HK1;HK1	0.107111075	2.175583894	0.444388102	4.015999173	2.090856211
HOMER1	0.623229276	0.12251564	-0.231757562	1.207017018	0.829397447
HTR6	0.390094958	0.895956603	0.013375526	0.679929247	0.73805284
IFIT3;IFIT3;IFIT3	0.847806907	0.942264662	-0.244369809	0.935748709	0.694596113
IFRD1;IFRD1	1.652050148	1.179944551	4.614667641	-0.15918902	2.107391003
IGLON5	1.463026441	1.767230032	1.783487274	1.098997076	1.053760573
ILK;ILK;ILK;RRP8;	0.099918	0.751570227	-0.226497641	0.758570288	0.697998512
INTS9;HMBOX1;INTS9	0.604712806	1.860748843	1.589212558	1.628146725	-0.059168087
ITSN2;ITSN2;ITSN2	0.762801266	0.763526845	0.054292123	1.854694356	1.924411828
JMJD8;JMJD8	0.102600827	0.68627902	0.326409584	0.679111099	0.745982036
KCNA1	0.497157635	0.60453448	-0.083492806	0.987549179	1.279727618
KCNK1	0.712285573	0.114414746	1.984300414	0.047754804	0.821419894
KCTD2;ATP5H;ATP5H	1.839281806	0.902641778	0.66737421	0.854181429	1.262779113
KDSR	0.432420763	1.904637105	0.964295032	3.435399674	1.603051793
KIAA0195	0.064052	1.275256873	-0.278597034	0.773696752	2.364261517
KIAA0232;KIAA0232	0.677493627	0.51957911	1.616574407	-0.151394272	0.860773958
KIAA1586	1.505163486	0.171452916	1.447440755	2.210369007	3.634539828
KIAA1712;FBXO8;FBXO8	1.671593852	0.847777594	0.381828437	0.467787392	0.781965594
KLC2;KLC2;KLC2;KLC2	1.423918951	1.324467859	2.07624321	2.076899901	-0.317023796
KLC4;KLC4;KLC4;KLC4	3.391379902	0.736366394	1.634410745	0.210856836	1.368962871
KLK9	0.174472134	0.638325085	1.485697431	0.633296015	0.266073952
KRT6B	0.102983869	0.829780348	1.478997453	0.599118064	-0.20643328
LCE2A	0.94688005	1.064630987	1.346102632	-0.14876446	0.119425525

LDLRAD3	0.929532367	0.26490451	1.026433959	1.047908214	1.653486805
LDLRAP1	0.827937179	0.544972851	0.646801877	0.536694482	2.086007598
LEPRE1;LEPRE1;C	0.575256911	0.751684254	-0.362797002	2.179703334	1.317143704
LIMA1;LIMA1;LIM	0.813807014	1.545311117	0.89662572	0.434007682	0.056592334
LIN54;LIN54;LIN5	1.19647126	1.265913089	0.609190978	0.850487543	0.60332867
LINGO3	1.163229676	-0.102753241	0.368009517	1.85147245	0.990680829
LITAF;LITAF;LITAF	0.646808703	0.612771453	0.439879046	1.767232647	1.311699641
LOC100133469	-0.159092186	1.482554154	0.631809251	2.34960936	1.193018005
LOC100270746;C6	0.944050358	2.428305879	1.87871385	1.853967645	-0.076051511
LOC100289511;SF	-0.512261708	1.203828925	1.23144034	2.15238446	1.125021461
LOC285830;LOC28	0.195764513	0.682786949	-0.022026468	0.759312337	0.639150917
LOC338799	1.226005438	-0.198268457	1.325178316	1.015505594	0.905648845
LOC441046	-0.322771368	0.88006479	0.954612444	1.075285316	0.740655856
LOC645323;LOC64	1.410262747	1.194816338	0.985884503	0.498820199	0.802221462
LOXL4;LOXL4	1.088213902	0.287153158	0.171014091	0.662957546	0.70216574
LRP1B	-0.007287467	0.446511322	1.413704146	0.772720188	0.628146697
LRRK2	-0.293610325	0.581921762	0.809565739	1.074611276	1.158936492
LRTOMT;C11orf59;	0.160210752	1.579103815	2.201509578	0.868458158	0.954217004
LSM14A;LSM14A;L	1.718666972	1.154286108	1.9554324	1.472727699	0.770258374
LYRM4;FARS2;LYR	0.778513204	1.075927674	0.374103297	0.214453731	0.846096915
MAGEE1	1.129650975	0.088353721	1.199329684	0.632606217	0.294858455
MALT1;MALT1	3.12964722	0.563752151	1.122533945	0.767825741	1.328748613
MAP3K7;MAP3K7;I	0.91374005	-0.045178911	1.852061431	0.62249955	0.505649658
MAP4;MAP4;MAP4	0.622255902	0.355288703	0.176085244	0.884331254	1.683096262
MARVELD1;MARVE	0.777501796	0.429398098	0.5187021	0.607539971	8.28163179
MBNL1;MBNL1;MB	0.912402824	0.983190774	0.872376474	0.473960072	1.161465629
MDGA2;MDGA2	0.35902188	2.059796406	-0.056743645	0.598039948	1.230982019
MEA1;KLHDC3;KLI	0.826057843	0.330239187	0.762229989	-0.012444797	0.622076213
MEAF6	1.146209751	0.650829023	1.083187216	1.358740513	-0.468134121
MED1	2.193019096	0.746345045	0.401003662	1.835929103	0.097973251
MED14;MED14	0.240961829	0.905623374	-0.081731567	1.230604165	1.108192937
MEIS2;MEIS2;MEI	0.826428274	0.882330984	0.914941544	-0.134831949	0.720783247
MEOX2	1.454881734	0.916913993	0.233392695	-0.177753524	1.461764843
METTL6;EAF1	1.033739714	1.803682614	-0.14429778	1.362536208	0.86312702
METTL7A	-0.021708805	1.640707861	0.775489281	0.924774666	1.991631061
MFGE8;MFGE8	0.079756649	0.517442339	1.37067136	0.74435195	0.806145172
MIR17HG;MIR17H	1.578814215	0.770919059	0.618736519	1.423222891	0.368130334
MIR1908;FADS1	0.593044637	0.580657008	1.016335495	0.622125445	1.699276603
MIR2110;C10orf11	1.194738994	1.316232621	0.046939203	2.567418664	-0.196088108
MLL5;MLL5;LOC10	3.091352974	0.717864801	0.250669648	1.777074965	2.732449459
MLLT6	0.123494425	0.619099028	0.70842868	0.840946893	0.439779319
MOSPD3;MOSPD3	0.274413787	3.065424399	1.753115348	0.444561034	1.812399791
MPPED1	-0.136128708	0.155312876	0.847488257	1.0186269	2.082352986
MRPL23	1.667718836	0.862655053	0.407454971	3.275638304	0.134815824
MRPS18B;PPP1R10	0.827695309	0.981049727	1.045456823	0.332787442	0.209169417
MRPS36;MRPS36	1.72126277	0.850023232	2.271861492	0.43871556	0.064223919
N6AMT2	1.077708806	0.814297444	0.053799862	0.117414962	1.116728463
NAA30	0.910532288	1.153350076	0.60993464	0.067818063	0.226256535
NEFL	4.354971789	0.283905306	0.842511245	0.40801291	0.960921536

NEK7	0.728782254	0.555609848	1.060517536	0.638808102	0.497088944
NFIL3	1.563279053	1.373121222	-0.30720208	0.853141005	0.596639289
NIPAL3	0.967011112	0.405104692	1.339094413	1.674781725	1.458875136
NLGN4Y;NLGN4Y;N	0.544817839	1.57335084	0.886489705	0.956242398	1.935749359
NSUN3;DHFRL1;D	0.621277252	0.712426396	0.630158817	0.530044184	0.754285365
NTM;NTM;NTM;NT	0.804293212	1.036197599	-0.45435649	0.669190838	0.5539197
NTM;NTM;NTM;NT	1.189611124	0.998805717	1.362688952	0.868636028	-0.011308776
NUDCD2;HMMR;H	0.749078292	0.784349302	1.07916499	0.584239752	2.693316925
NUDT6;NUDT6;SP	0.322819661	0.878910063	-0.008046873	0.705549969	1.205508495
NUP35	-0.338657663	0.754840292	1.046162842	0.639640642	1.307032452
NUP43	2.407279666	1.229012438	0.66407108	0.509452267	0.571475228
OBSL1	-0.045234468	0.653067906	0.525031621	0.697148423	1.26290363
OCA2	0.27641365	0.91335964	1.574128683	0.409346225	1.254448978
OR8S1	0.312936756	2.189149077	1.470389224	1.928850139	0.622414183
ORMDL2;SARNP;S	2.351497425	1.367494448	1.332244149	0.507849463	1.918055576
OTX2OS1	0.055150076	1.232691067	-0.474168965	0.994991066	1.067825427
PAFAH2	0.165851737	0.599002557	0.315726207	1.377578	0.78649907
PAX3;PAX3;PAX3;I	0.402467633	-0.17407154	0.723920067	0.633958286	0.639777214
PBX4	-0.020137704	0.617203245	0.476444972	0.754623951	0.797620553
PCDH19;PCDH19	0.608198256	1.464815458	0.012156127	0.913524379	0.910122887
PCDHB11	0.126396795	1.012519688	0.240073029	1.858990497	1.087940879
PCDHGA1;PCDHGA	0.641392026	1.768730058	-0.068350219	1.32542573	0.915906629
PCDHGA2;PCDHGA	0.379088954	0.948109099	0.943149983	1.984581996	0.187764936
PCGF2	2.813080899	2.101193076	-0.49269551	0.219991879	2.275672677
PDHB	0.613691667	0.575413595	0.825739918	0.461843941	0.667094982
PDIA6	4.858177255	0.665544423	0.719409417	0.502636987	3.128655223
PDYN	0.143062708	0.065459076	1.081768132	0.75569509	1.245358698
PERP	0.745485868	0.812264091	0.788738136	0.831633332	0.549664381
PGAP2;PGAP2;PGA	0.111079153	1.024462383	0.523364645	0.871641215	0.93992719
PICALM;PICALM	0.785437647	0.527219815	1.024313322	0.934521401	0.090791051
PIK3R3;PIK3R3	0.491171094	1.18697647	-0.031485227	0.964258739	0.828019186
PMS2L2;STAG3L3;	0.631516333	0.05321206	1.815493049	2.135718055	0.646340392
PMS2L3	0.705946458	1.428969654	0.071276967	2.803278852	-0.448558064
POPDC2	0.461054984	0.756390033	0.68922048	0.815656868	1.326734208
POU6F2;POU6F2	0.304367398	0.822952321	0.090783248	0.906177199	1.137544796
PPP1CB;PPP1CB;P	-0.028537483	-0.040868498	1.622162291	2.089584625	2.218681557
PPP1R12A;PPP1R1	1.124506989	1.868501507	1.145313164	-0.114334628	0.126959599
PPP1R15B	0.576673903	-0.356454266	2.440748751	2.205672508	0.933052497
PPPDE1	0.950024293	0.177032327	0.453327075	0.968434813	1.226729819
PRAGMIN	1.340938922	0.103288943	1.034353631	0.866585953	1.897342306
PRDX1;PRDX1;PRI	0.884038813	1.441246368	1.406199131	0.461693054	-0.314858765
PRDX3;PRDX3	1.129291385	0.838331541	0.14880928	0.502398512	1.170877274
PRKCH;PRKCH	1.077736237	-0.156008326	2.053012267	2.295268127	0.271487421
PSD3	1.188838115	1.600695845	0.3751107	0.278005151	1.067895634
PSMD9;PSMD9	0.694662972	1.229227975	-0.053046799	0.605704377	0.581898059
PSMG2;CEP76	0.801272862	2.378965909	0.521115106	0.65255761	4.987183661
PTGER4	1.544149466	0.262275425	-0.431714288	1.229690085	0.959075359
PTPRS;PTPRS;PTP	0.226849985	0.54757895	0.607551732	1.48916615	1.43114558
RAB43	0.892019477	0.680924307	1.245430457	0.285376023	0.435083965



RAB7A	0.989825539	0.894999569	0.265294979	0.163450768	0.751306638
RALGAPA2	-0.062263389	1.073437344	0.978762136	0.67888056	1.019754439
RANGRF;SLC25A3	1.271944769	0.525804276	1.010366119	0.730238454	0.287879495
RASGRP2;RASGRP	1.341211114	1.14762093	1.383353836	0.283305908	1.216999835
RBAK	2.426753878	0.072567495	2.213831347	0.783042789	0.131910904
RBM24;RBM24;RB	0.499170536	1.813723757	0.125078787	0.939118553	1.415959752
RBM28;RBM28;RB	1.773210099	2.447220486	0.737017677	0.745320772	0.477110809
RBMS1;RBMS1	1.740105734	0.606378108	-0.106740581	0.740161346	0.948829897
RCAN2	0.770009495	2.18718391	0.602850099	1.282010688	-0.162236785
RCE1;RCE1;C11or	-0.375434348	1.212105211	2.12011516	1.408619085	0.677957695
REER;REER;REER;	4.431921192	0.913370789	0.945451941	0.951835469	0.779116084
RGL2;RGL2	0.269372964	0.435594009	1.015683815	1.221952736	0.913902367
RGS7	0.717778221	0.645551224	1.801759863	0.522487663	0.969955678
RING1;RING1	2.101260853	1.054009552	2.570638797	2.305249076	1.556309338
RMND5A	0.92767877	0.815104001	0.455114662	3.925145183	-0.099130351
RNASE4;ANG;ANG	0.992266097	2.08925185	1.222708028	0.020022776	0.193878201
RNASEH2B;RNASE	1.288512636	-0.012366807	1.025677162	1.314020148	1.509192454
RNASEK	0.5971093	0.023955829	1.185671125	-0.088444294	1.345224265
RNF11	0.339185948	0.688266477	0.56280809	1.052318555	0.989675013
RNF181	0.941731611	1.744751507	0.480729475	1.03517692	0.99745318
ROCK2;ROCK2	3.091127772	0.965900059	0.447590385	1.093893844	0.150937251
RUNX1	0.033586722	0.89286387	0.413344159	1.44246762	1.084687742
RYSR2	1.96173023	0.771834706	1.161114957	1.334308641	1.883220835
S100A11;S100A11	1.900888426	-0.062807231	0.539074411	1.88950863	0.972451045
SAMD14	2.178485308	0.870412872	2.006146935	0.205900058	0.885870356
SAMD9	0.478621715	0.851323539	0.047696421	1.110226385	0.894242257
SCARB2	1.584808434	0.68504173	1.469555557	0.094112505	0.278173825
SCIN	0.063909295	1.369322778	0.648015744	0.354283385	1.244841525
SDC4	0.457119811	0.874448524	0.984560911	0.897769379	-0.046563468
SDHB	-0.009267543	0.738983056	0.275040551	0.81421544	0.993742078
SETBP1;SETBP1	-0.323833546	0.667780593	1.216290827	0.895006557	1.001282547
SF3A1;SF3A1;CC	0.165851498	1.144421469	1.484269083	1.469254349	1.39296142
SFMBT2	1.173629499	1.759401172	1.226714361	0.437578419	1.52628187
SFRS18;SFRS18	0.916110145	1.086280442	-0.673425205	0.899903382	0.614711764
SH2B1;SH2B1;SH	-0.274807951	0.950019711	2.901768112	0.993065947	0.763559322
SH3PXD2A	5.323679804	0.60388805	1.263686048	1.577310692	-0.252803015
SHC1;SHC1;CKS1	1.537509388	0.211337071	1.422828705	0.827116608	1.003511828
SIK3	0.78969937	0.858415418	0.217523643	-0.271296842	1.244231796
SIM1	0.126234735	1.45482279	0.762400988	1.741528542	1.663538737
SIM1;SIM1	0.72141502	2.436697858	-0.053947338	0.729711745	1.83012319
SLC45A3	1.052101921	1.581466366	0.405292809	1.779741782	0.910262423
SLC7A5P2	0.567601316	0.910040989	5.376326222	2.531936391	1.921525935
SLC9A9	1.809615655	1.588065	1.534951437	0.137229029	1.147883133
SMARCA1;SMARCA	-0.28883654	0.132083297	1.202133685	0.898866099	0.667552043
SMARCC2;SMARCC	1.640862129	-0.062233011	0.861080852	0.972312327	1.815132742
SMS	0.617750094	1.529288864	1.354921279	0.402901663	2.299237745
SMYD3	0.41617476	1.525353291	1.142624277	-0.43153727	1.879778623
SNORD104;SNOR	0.493083453	0.713168154	-0.489057187	1.076682247	1.457705498
SNX31	0.386525163	0.250743618	0.750682284	1.314459415	0.967965548

SNX8	0.481667642	1.96301434	1.650859099	4.789465417	0.228857094
SPRED2;SPRED2;S	0.00941278	0.618440451	0.924808817	1.572064495	2.337814766
STAR;STAR	-0.342150011	1.373037198	0.894746831	0.757425283	0.678484161
SULF2;SULF2;SUL	1.509216347	1.870935261	0.910966879	0.200546282	0.910097578
SYTL2;SYTL2;SYTI	0.589314398	1.458387157	0.755100859	1.284341078	0.696968197
TAOK3	-0.237207893	1.005249607	0.668664187	0.74442854	0.226633671
TBL1XR1	0.179418046	0.697592386	1.719233032	0.067801478	1.424621974
TBR1	0.30335533	1.003828473	1.595132273	0.670438193	0.293432585
TECR;MIR639	0.70365725	1.464163028	-0.628239634	1.210187259	0.634415591
TELO2	0.943491289	0.090824587	0.224247152	2.122042778	0.60211196
THOP1	-0.227489871	2.62514642	0.993621498	0.655045631	0.444185023
THRB;THRB;THRB	0.73823098	1.065442945	0.192248919	0.795464575	0.470491374
TLCD1;TLCD1	0.969196404	0.804108	-0.081050204	0.300269201	1.160879349
TMCO1	-0.296726362	0.696755231	0.352317448	0.742663695	0.650882475
TMEM120A;TMEM1	0.927721685	0.07785131	1.061355942	-0.259472703	1.16651069
TMEM129;TACC3;T	1.404311578	1.070604124	2.671582814	0.505105371	0.657276606
TMEM187;HCFC1	0.146241447	1.797177262	1.691858341	1.211030001	-0.529765607
TMEM201;TMEM20	-0.073595672	2.738210712	0.902033511	1.487331893	0.54774766
TMEM57	0.765624781	3.500702352	2.179029244	0.582533695	1.531706973
TMEM65	-0.067286249	-0.148989026	1.936883664	2.063242778	2.182041317
TMEM67;TMEM67;	-0.087773241	1.620615491	0.852922572	1.62444006	0.230218154
TMEM97	0.389909464	1.144701946	1.279879404	0.486828289	1.028049134
TMOD1;TMOD1	1.532913224	0.725659583	1.426170481	0.607046917	2.078126799
TMSB10	-0.184625464	1.644921313	0.757469586	3.502544154	2.322153713
TNKS2	3.316585978	0.530788565	0.803059255	0.701884638	1.330230678
TNRC18	0.035147025	0.667708115	0.095393854	1.559247518	1.341876913
TOPORS	-0.44990075	4.841259974	0.289992712	2.455221925	3.957729671
TSC22D1;TSC22D	-0.249001844	0.476298407	0.863129879	0.748953882	1.500659402
TTBK1	-0.278079765	0.578315856	0.74111613	0.74047015	0.96041062
TTC15	2.693159201	3.712224092	-1.878992332	3.99625518	0.723372808
TTC31;CCDC142;T	0.587097029	1.376634915	0.603071938	0.207771636	0.679822081
TUBA1A;TUBA1A	2.483126131	3.231255204	-2.163075933	2.300967419	1.386745361
TWF2	0.596480728	0.757069577	1.224455261	-0.109683312	0.955410309
TXNDC6	0.609309066	0.573861059	0.03963682	0.647670433	0.615688899
U2AF1;U2AF1;U2A	1.069067578	1.781460863	0.933715188	1.339983536	0.198854951
U2AF2;U2AF2;U2A	0.051089515	0.985352572	0.943802202	2.496040028	1.214722565
UBE2CBP	0.554825009	1.336167028	1.147974726	-0.037895672	5.67146429
UBE2H;UBE2H	1.871872673	1.652446894	0.460709973	-0.356258196	1.408240115
UNC5A	0.262487058	1.242596089	1.103469739	0.276262178	1.823844172
USP31	1.119694477	1.31977797	-0.021321061	0.22238937	2.304280286
USP49	1.198406717	0.891637097	0.993526503	0.806312945	-0.153205271
VCL;VCL	1.496057686	1.421201834	-0.008383841	0.173975689	1.018865296
VIM	0.256927601	0.631683986	0.80050363	1.088327178	0.805105962
VRK2;VRK2;VRK2;	1.037082321	0.51961902	-0.121061556	0.757259462	1.779008518
WDR89;WDR89	0.595768264	0.82741586	0.042795453	0.194737394	0.735049696
WIBG;WIBG	0.733919889	1.729582704	0.044281402	1.381091557	1.607071851
WNT5A;WNT5A	2.980507772	1.815868248	1.80667411	-0.124376501	2.564271443
WWC3	1.005528179	1.153615592	-0.159680005	0.810878688	0.981752707
YIF1A	0.62026213	0.741487674	0.9936362	0.821182097	-0.059796092

YME1L1;YME1L1;M	0.692277369	0.607815152	-0.168576843	0.745739521	0.207857602
ZBTB33	0.416271163	0.601235315	1.070482404	0.404640812	1.407611939
ZDHHC13;ZDHHC:	0.592702288	0.678626226	-0.254310286	0.87181944	0.476000373
ZFYVE1	0.535724637	1.145670618	0.776000701	0.356719087	1.4065782
ZFYVE28	0.721332684	1.639991511	0.187388416	0.226058665	1.44445817
ZHX1;ZHX1	0.344707484	0.672302898	0.180946502	0.904154596	1.650280185
ZIK1	1.944795399	0.410680267	1.931198481	0.229902878	1.679397371
ZNF207;MIR632;Z	0.590802856	0.016538961	0.926662869	0.944884899	0.262202321
ZNF259	-0.077543745	1.327717886	1.421266829	1.419804713	0.548431819
ZNF416	0.700168444	0.953456205	0.402705885	-0.278273912	0.846070658
ZNF488	1.057659976	2.563201836	0.198276388	0.483516643	1.284974515
ZNF764	0.659637884	-0.034370159	1.531037985	4.44660194	4.077300633

hypomethylated

gene symbol	log 2 ratio AR Day 1	log 2 ratio AR Day 3	log 2 ratio PSA Day 1	log 2 ratio PSA Day 3	log 2 ratio PSA Day 5
AARS2	0.35251289	-3.869670423	-0.994076663	-3.703183456	-4.513349651
ABCG4	-1.050304934	-1.134733066	-1.166725199	0.030613136	-0.638777811
ACBD5	0.146641118	-3.262750076		-1.937676692	-1.830735224
ACTR8	-0.350193844	-1.050136954	0.134868097	-1.287540001	-1.126722389
AK7	-1.299484858	-2.509623068	-2.604310395	-0.691846916	-0.734780783
ALG11	-1.103820761	-6.071229969	-1.122094205	-0.374147642	-0.751614088
ANAPC11	-0.280890734	-1.790307257	-3.5853731	-1.308470331	-1.28026537
ANO1	-1.430038464	-2.486739597	-2.108814658	0.346047072	-1.89899883
ARL4A	-1.259887691	-2.037438405	-0.487225258	-2.259633068	-0.138625325
ASH1L	-1.649249878	-0.132419282	-1.351304902	-0.852648548	-1.761614738
ATG4B	-0.513463126		-1.577488458	-1.118792055	-0.029330594
ATP2C1	-0.904168517	-1.274090309	-2.077391252	-2.643223732	-0.424251308
B4GALNT4	-0.526596419	-1.166525355	-2.225210914	-1.304919645	-0.548083336
B4GALT4	-2.577071095	-1.32803912			-1.391042506
BACH2	-1.432303742	-0.017535151	-1.097755019	-2.167940506	-0.943417747
BCLAF1	-0.160303146	-0.59339448		-1.430009945	-1.677881453
BET1	0.118305851	0.081260133	-2.04716985	-1.516487339	-1.1548061
BEX4	-2.900617065	-1.860475099		-3.11591229	-0.523984435
BTNL3	-1.782316925	-2.406979551	-0.611199672	-2.221563272	-0.67285097
BUD13	-1.195225596	-0.796529092	-1.19933812	-6.141730964	-0.438742842
C10orf4	-1.206001921	-1.516589557	-0.364016453	-3.803275217	-1.196524722
C10orf41	-1.778537164	-1.869266568	0.453685077	-0.23363018	-1.386880443
C11orf71	-1.013051973	-1.968267032	-1.187110387	0.538668057	-0.424812931
C11orf91	-0.345294783	-0.297920874	-1.415496796	-1.620015739	-1.220769986
C12orf29	0.058318687	-1.735645238	-5.597117613	-5.645904893	-3.321903576
C12orf44	-1.760193178	-0.16266578	-3.040517633	-2.334968619	-0.378403367
C14orf104	-2.330108204	-1.202176945	-1.275152833	0.136016883	-0.553659708
C16orf42	-1.256099253	0.179607927	-1.755593972	-3.64517254	-0.754640972
C19orf26	-1.128811251		-1.131798055	-2.009100457	
C1orf130	-1.324051973	-1.44575568	-2.145789039	-0.754999111	-0.440623808
C1orf69	-3.406013258	-1.124800611	-0.707239332	-1.165753744	-0.566430812
C20orf43		-5.789527948		1.001647664	-0.884452272
C20orf56	0.242045161	-1.068636373	-1.08751073	-1.99914701	-0.885681111
C6orf153	-6.390881301	-4.669091098	-2.486530343	-0.221612795	0.531877707

C7orf68	-1.044713647	-0.402758619	-1.658745235	-1.293604018	-0.05530425
C9orf95	-3.700501136	-3.158679565	-0.452003085	-1.576713852	-1.15210884
CA5B	-1.845026136	0.441411446	-1.483406838	-2.039777201	-0.828766098
CACNA1A	-1.282773343	-2.106132441	1.404100427	-3.093168806	-1.698293096
CALCOCO1		-0.631493744	-1.087556601	-1.069874479	-2.452736255
CAMSAP1	-2.325785882	0.559256247	-0.749468288	-1.082272889	-1.44254068
CELSR3	-1.527152692	-1.042135995			-3.674894989
CHSY1	-6.657940784	-0.043569898	-1.249523082	-2.967133288	-6.563990563
CLCN6	-1.695588756	-1.369672247	-0.488017671	-1.472725503	-0.017372951
CNOT2	-0.272698093	-1.14504115	-1.314687168	-0.372569485	-1.468231795
COL23A1	-1.196566471		-1.259644037	-1.86612777	-2.126237543
COL7A1	-0.458238913	-3.649145912	-4.616520956		-2.26070581
CPLX2	-1.547199108	0.208201725	-1.948913461	0.199376225	-1.146956373
CR1L		-1.508002783	-2.291479595	-2.123922861	
CRHR2	-2.239209347	-0.070516118	-1.334849158	-1.473930202	-2.11368508
CRK	-1.335316209	-0.421203468	-1.250082961	-0.435229987	-2.060807356
CSNK2A2	-1.669864892	-1.018989137	-2.210599387	-1.07228229	0.01763621
CST3	-1.133886155	-1.0917904	-0.550132193	-0.750805731	-1.308592939
CTHRC1	-1.17851681	-2.829957675	-0.540095785	0.348353744	-2.26017617
CUTA	-0.011007408	-1.400337222	-3.228546563	-2.702016489	-0.788983781
CYP26C1	-1.773345797	0.043932969	-1.018007995	-1.237491089	-0.814025963
DDAH1	-0.070991878	-0.55534712	-1.668221324	-1.058370482	-1.411026684
DDX6	-2.389484587	0.154397407	-1.219223309	-1.351190767	0.166091009
DEM1	-1.114897981	-0.530098171	-0.864000677	-2.119109753	-1.769168746
DGAT2	-4.511260904	-1.082555894	-0.051861523	-1.273653934	0.144265586
DHRS7C	-1.051378543	-0.182314147	-1.205472759	-0.411934443	-1.596808912
DLG4	0.10535516	-2.58880707	-1.333746478	-1.138751449	-0.989576276
DNAJC16	-1.029592957	-0.852615025	-1.54901983	-0.487891046	-1.018171399
DPH1	-1.607703936	0.329508554	-1.139879459	-1.049420363	-0.427634484
DPYSL4	-1.111476063	-1.052898763	-1.261700009	-0.278694254	0.083564653
E2F5	-5.386949065	-1.260933402	-1.350461388	-0.3828029	-0.643880919
EFNB2	-1.002602503	-1.567513339	-0.034330527	0.006370499	-1.12332157
ELOF1	-1.380029991	-0.774238312	-2.024999962	-1.860879987	-0.132102945
ENOX1	-0.001388577	-5.667526277	-4.413699167	-0.447557727	-1.330172173
ETV1	-0.052061538	-1.774228709	-0.400163377	-1.616538958	-1.27132487
EVC2	-0.552848273	-1.960638464	-3.837193817	0.430654583	-1.516795132
EXOSC6	-1.155448033	-1.132910116	-5.079887578	-1.245066487	-0.560204973
FAM104A	-3.423643452	-0.68569415	-4.146202258	-1.061846759	-0.043634761
FAM117A	-0.90341265	-0.545631277	-1.818735184	-3.362032273	
FAM168A	-3.081302868	0.340112098	-4.706898996	-0.204468015	-1.558947365
FAM174B		-1.460725806	-1.812229029	0.203688373	-1.51968515
FAM35A	-0.963100846	-1.061399302		-1.150157468	-0.728531405
FAM49B	-1.411088754	-4.111480557	-1.74847614	-0.415366669	-0.796376528
FAM69C	-0.257984604	-1.138725398	-1.123374817	-0.968165235	-1.029491516
FAM82B	-0.862600828	-1.487661485	-0.76840762	-1.522471412	-1.602624285
FANCF	-2.618455301		1.44449522	-2.452909771	-1.997983496
FBXL16	-1.626226546	-0.629220777	-3.271126059	-0.080899642	-1.097709088
FJX1	-1.259655852	1.553708998	-2.876415332	-0.957250485	-1.146020417
FKBP8		-1.20026786		-1.153483753	-2.112380014

FLJ10661	-2.036950102	-0.449360741	-2.198199487	-0.436711073	-1.830434789
FMNL1	-5.418823631	-1.188286698	-1.171896509	-0.03523151	-1.436433727
FRS2	-1.962765698	0.45659447	-1.63505029	-0.972284901	-1.997601933
FRYL	-1.168869887	-1.556029852	-2.1596883	-0.206708286	-0.512781311
FSTL4	-1.53809782	-0.77266717	-1.182586394	-1.097655149	-0.77176174
FXC1	-1.399429208	-1.370131456		0.102192063	-1.10904826
GABPB1	-1.060609221	-1.102052422	-2.751635645	-1.679850165	-0.531805268
GADD45B	-1.331174492	-0.037877402	-1.991701033	0.171915432	-2.102259871
GLA	-1.378753801	-1.617808691		-1.357838166	0.084002578
GOT2	-1.267299827	-0.299304197	-2.165194867	-1.460123135	0.062761875
GPR161	-0.561953087	-2.258070944	-3.777165214	-0.211760635	-1.680971041
GRIN2A	-1.386077689	-2.062190791	-1.719318972	-1.673730978	-1.57682871
HCCA2	-0.561125782	-1.193267982	-1.86927555	-0.072898709	-1.484339229
HDAC5	-1.26618694			-1.522578911	-4.157834223
HEXIM2	-1.299129325	-1.275090574	-0.466239821	-0.238323239	-1.010223953
HIST1H3B	-0.545206432	-3.479979591		-1.308935805	-1.717944983
HLA-DPB1	-0.792576719	-1.977951687	-2.574666867	-1.18229857	-1.101991263
HMGXB4	-0.287796736	-0.50516113	-1.04544939	-1.098830122	-1.053898636
HMOX1	-1.11127816	-2.61673051	-1.492453451	-0.508915712	0.093338637
HNRNPH1	-1.128636471	-1.146806917	-1.688420632	-0.933906692	-0.976790898
HSD17B1	-0.61043801	-3.237357992	-1.364775472	-0.46466071	-1.193653541
HTR7P	-0.781925236	-1.516239098	-1.369188108		-0.55522753
IGF1R		-2.952286465		0.988552458	-0.585464327
IRF6	-0.576897831	-1.229336787	-2.059400266	-1.143236793	0.283368178
IRX2	-0.182195222	-3.93840034			
ISCU	0.474819855		-1.720596905	-0.767495834	-2.648419246
ISM1	-1.664404932	-2.240233736		-0.631841265	0.349732639
KBTBD4	-1.007318726	-0.382448416	-3.492894535	-1.382979063	-0.781255116
KDM6B	0.281173206	-2.241690154	-1.121393018	-0.559988275	-1.08380118
KIAA0101		1.612880518		-1.446882614	-1.809623897
KIFC3	-0.823642625	-7.025812663	-1.844174313	-0.987940335	-1.234286019
KLF6	-1.190285162	0.209767744	-1.082617177	-0.848542104	-2.261884766
KRAS		-4.937931797	-3.532743703	1.05856053	-1.155297075
KRTAP10-8	-2.731935561	-1.113080603	-0.094354551	-1.139300496	-1.711337777
L1CAM	-2.719164911	-1.551306519	-0.771793262	-0.345371439	-1.269455007
LARP1B	-1.086364681	-1.652535866	-2.663399048	-0.541614024	-0.600310935
LGI4	-1.114911211	-1.235343515	0.291329805	-0.891978174	-1.157462295
LHFPL5	-1.559371607	-2.387421511	-0.501969435	-0.660625669	-1.291322413
LIN52	-1.113107264	-2.300022395	-1.014976253	-2.850341869	-0.383184396
LMBR1	-1.119571287	-1.799581929		-0.536503963	-2.600312425
LOC100128164	-1.86954971	-0.369881884	0.155037465	-1.323784315	-3.623892874
LOC100133957	-1.069785616	-1.602427601	-2.061031525	-0.130821289	-0.526134257
LOC100289341	-1.905928013	-1.418826328	-0.281456159	-1.747252943	-1.700324182
LOC100302652	-1.347872877	0.249040784	-1.033613306		-1.968940085
LOC285830	0.829822943	-1.156165048	-1.405634458	-1.752351066	-0.418914234
LOC389765	-0.26299624	-1.081395878		-1.262727911	-2.509887764
LOC404266	-3.274545837	-1.01939395	-0.28852115	-2.013778095	-0.535194996
LOC492303	-3.07359405	-0.54936607	-1.284744667	-0.392232159	-1.210698902
LONP2	-0.778676642	-1.7626684	-1.428801884	-0.76894016	-1.009689816

LPHN1	-0.757222135	-0.252384248	-2.95713012	-1.342664368	-2.766265074
LRCH3	-2.481617796	-1.406963088	-1.430913443	-0.484185449	-0.203162092
LRTOMT	-1.146276743	-1.340711898	-0.095447544	-2.356498337	-0.468105862
LZTS2	-1.774950892	0.251049609	-1.601646143	-1.948902625	-1.108950138
MAGEB6	-1.712828615	-0.443275907	-1.390143099	-1.207804624	0.094718717
MALAT1	-3.128135692	-1.109987257	-0.364993287	-1.210682855	
MAVS		-0.832853859	-3.796161646	-0.538140796	-1.365393314
MBTD1	-1.318383785	-1.037916255	-2.414210005	-0.648054505	0.135617263
MED25	-0.211512377	-1.763110727	-3.828413948	0.233761615	-1.348988084
MIR548H3	0.85711943	-1.17626184		-1.296229091	-4.096766628
MPI	0.15074082		-1.595299941	-1.685468989	-3.00205362
MPV17L2	-1.4237918	-2.560463281	-0.96832315	-1.015055292	-1.921870567
MRI1	-0.380894645	-1.722632555	0.119100547	-2.137583183	-1.638695362
MRPL28	-1.32688481	-1.34002461	-2.835395147	-1.160595935	0.18079766
MST4	-0.350288158	0.529266197	-1.901009362	-3.914356486	-1.788292699
MTCH2	-2.377844832		-1.318930968	-2.036250575	-0.089074918
NAAA	-1.282923797		0.762392732	-2.657880366	-2.324680364
NBPF3	-0.722477815	-1.933824497	-0.50395439	-1.046005838	-2.163668648
NCAPD2	-1.856019368	-0.088624716	-1.993878122	-0.365090648	-1.553113602
NCKAP5L	-0.316717354	-3.938508722	-0.286436319	-3.047014933	
NDE1	-1.745073264	-0.786138092	0.14638418	-2.458215877	-1.019173512
NDUFS1	-4.042745297	-1.262411063	0.041002604	-1.627890128	-0.029818969
NETO1	-4.519730532	-3.360209026	0.911403014	-0.605314309	-1.263180399
NMUR1	-1.0791161	-0.455413861	-1.011196983	0.020111692	-1.207447314
NOM1	-2.711769729	-1.869141043	-0.904948418	-0.640406904	-7.884143144
NPHS2	-1.677826418	-1.204758708	-1.031876344	-0.557066796	-0.812034406
NRBP1	-2.12448369	-1.001306393	-0.85441619	-1.350027314	-0.206382189
NRXN1	-0.062793263	-1.433162357	-1.651715379	-1.026708969	0.060330052
OSBPL1A	-1.741765862	0.474577461		-1.124727089	-5.418990729
OTUB1	-4.494349011	0.556855084	-2.485528723	-2.781354835	-1.668355207
PASK		-1.352182495	-5.350262871	-1.383371068	-3.055205008
PAX2	-1.68445659	-1.230501098	-1.199917185	-1.297432517	-1.358896797
PCDH8	-1.430628654	-2.003637351	-1.213363228	-1.747751942	-4.041957486
PLEKHG5	-2.038583471	-0.751533377	-3.439036339	-0.655125548	-1.17854347
PODNL1	-2.353861353	-0.848610662	-0.190764332	-2.618405256	-2.587650113
POLR2J	-1.24417664	-2.297606693	0.084482644	0.199274102	-2.247013117
PPWD1	-0.64465732	-1.447586343	-1.124876611	-0.473823342	-1.964022352
PRDM16	-0.775381252	-0.664333783	-1.097803252	-1.752718225	-2.119462086
PRRG2	-2.991720642	-2.044855586	-0.531690713	-1.000536105	-0.273700537
PSMD12	-0.716178683	-2.9837947	-0.337498479	-1.519626601	-3.261158224
PTPLAD1	-1.45331621	-1.010601123	-0.304482938	-1.387141721	-1.110979313
PTPRZ1		-0.781514266	-1.633964662	-1.307241521	-2.197765724
RAB8A	-1.264359323	0.004118563	-1.919798083	0.116448679	-1.173056895
RABL4	-0.918033073	-3.776634494	-1.594100056	-0.211297336	-2.081293158
RAI14	-0.21907157	-1.515861282	0.31256286	-1.271546194	-1.280890304
RASA3	0.13969	-1.487288995	-1.499696425	-1.265327639	-1.33931671
RASL10A	-2.579843212	-1.158686072	-1.402786242	0.032804224	-0.384862484
RAX	-3.957170124	0.652369367	-1.740635575	-3.047623349	-1.318440591
RILP	-1.545226266	0.046676834	-2.720283949	-0.639045346	-2.459855988

RNASEH2B	-2.363533059	-2.389342879	-2.034109474	1.188327684	-0.949050971
RPL36AL	-1.916801386	-3.58364702	-0.035872902	-0.819902769	-1.89186687
RPLP2	-5.045256753	-2.566167698		0.548005013	-2.508512314
RTBDN	-0.519636149	-1.700222198	-1.772838501	-2.034378291	0.071504208
S100A6	0.561548628		-6.3122846	-1.312784157	-2.144543367
SAFB2		-2.011692071	-0.214582378	-1.171166795	-2.16602424
SARS	0.143254797	-0.76303857		-2.349484286	-1.500794124
SCAF1	-2.019077343	0.511239324	-1.473102248	-1.606364684	
SCAI	-1.453426056	-1.795063505	-0.928878692	-0.320727029	-1.624087787
SCAMP1	-1.175223108	-0.761911095	0.139516175	-3.207658625	-1.569834835
SCHIP1	-0.221764752	-1.498188597	-2.225032334	-2.384677797	0.523857952
SCYL3	-1.829827071	-1.11287827	-0.282490384	-0.861056455	-1.729057532
SDHAP3	-0.591303296	-2.142693128	-7.285186128		-1.032828784
SEC61A1	-2.611779885	-0.085774051	-3.741442484	-1.000782035	-0.463894472
SEMA4F	0.190295398	-2.255515303	-1.042681504	0.279104855	-1.140830652
SFRS6	-1.371157909	-1.990687979	-0.83101295	-2.322690706	0.519361151
SFXN4	-1.520580458	-4.164859304	-0.619934987	-2.1807839	-3.245659053
SGSM1		-3.572574194	-1.060549713	-1.440454767	-1.270851703
SHCBP1	-1.54587722	-3.457913298	-0.93857841	-0.529989459	-1.146282655
SLC10A7	-0.376307778	-2.55633723	-2.596223294	-0.201540651	-1.078413987
SLC1A2	-1.560290028	-0.348607618	-2.030355504	-1.657492737	
SLC25A21	-1.178710753	-2.653050052	-4.476695095	-3.762196787	-0.221508743
SLC35E3	-0.48116841	-0.635609665	-1.387486679	-1.449610872	-1.295962608
SLC38A1	-1.680269892	-1.393241893	-2.556583763	-0.087259789	-0.370644824
SLC43A1	-0.342983417	-0.588663545	-1.973123063	-2.562030378	-3.454824465
SLC4A1AP	-0.185706502	-1.627207498	0.064139298	-1.305428173	-1.100543225
SLC9A3	-1.46527444	-2.198159813	-0.513726546	-0.230269129	-1.099795981
SLCO5A1	-1.370689648	-2.036506177		-0.264207275	-2.498223728
SLIT1	-2.611935627	-1.540897532	-3.01611312	-1.643605426	-2.603773621
SMARCD1	-1.345463101	-0.322111437	-4.449808397	-1.018274634	0.18087272
SPPL2A	-0.886843829	-1.043087826	-2.124547908	-2.347730146	-0.96944724
SRP72	-0.067262092	-1.081231154	-1.564422896	-0.514368647	-1.190620394
SRRM2	-0.821636159	-0.671910704	-1.182582873	-1.303244751	-2.815834331
STL	-0.214454848	-0.718768118	-1.977366732	-3.161839741	-1.259886904
SUCLG1	-2.013989079	-1.153374773	-1.01381286	-1.201241111	
SYCE2	-1.724244227	-1.234834297	-0.11098229	-3.24996746	
TAPBP	-2.011897653	-0.001970377		-3.415125646	-2.335358918
TCEAL6	-3.199904882	-1.061518791	-1.394094567	0.222044072	-1.046823906
TECR	-1.5318004	-1.004533252	-0.097148212	-0.459261966	-1.092344394
TGM2	-1.329246877	0.675505769	-1.117836938	-1.186399229	-0.671893069
THOC2	-0.041601932		-1.203500057	-4.150581411	-3.317764549
TMEM111	-2.083270131	-1.09189756	-1.111402282	-1.156407683	0.259586815
TMEM179B	-1.464790861	0.387110949	-1.265228726	-1.292669816	-0.580832011
TMEM185B	-1.417569194		-0.240456821	-1.429345841	-4.953942402
TMEM53	-0.430168203	-7.277214109	-2.960514203	-0.045034916	-1.091108053
TNFAIP8	-1.177479486	-0.21978824	-2.106641978	-1.891852669	-0.344830685
TRAPPC1	-0.398228309	-1.187897216	-1.505600937	-5.400908473	-0.882190078
TRIM41	-2.882950673	-1.431184914	-0.326502098	-1.161809321	-1.762310406
TSSC1	-0.485717398	-1.059447371	-1.248077849	-1.130859745	-1.885077361

TTC19	-2.283767095	-0.361309864	-1.015458977	-1.517483928	-0.783008256
UBP1	-1.198230236	0.745391024	-1.205482083	-0.730329279	-1.399831462
URB2	-1.33011725	0.141209576	-2.443430653	-1.443877737	-0.112704361
USMG5	-1.71521644	-2.620780651		-2.685723029	-0.054525301
USP48	-1.078604635	-0.941819134	-2.662397154	-2.669782977	
VPS41	0.811259764	-1.33729366	-2.262788335	-0.640505824	-1.048412933
VSTM2L	-0.815426733	-0.034750347	-1.433534642	-6.893175321	-1.079311858
WBSCR22	-2.207387083	0.034994587	-1.042066292	-0.528234619	-1.191756913
YPEL2	-0.524549084	-1.400489342	-1.344560737	-1.006588518	-2.554082531
YY1AP1	-3.847805606	-1.16456708	-0.491731275		-0.903627192
ZBTB12	-3.814153248	-0.996354969	-1.538506811	-1.047626716	-0.778787602
ZBTB22	-1.625653306	-1.479457232	-0.283828224	-0.84951308	-1.257882181
ZBTB4		-0.13318674	-2.382706482	-2.93311893	-1.282067549
ZDHHC19	-0.865199953	-1.079925387	-1.987766063	-1.237729451	0.317171398
ZIC4	-1.099049967	0.386905613	-6.667064305	-0.764136601	-1.095891277
ZNF248	-6.158827142		-0.557938983	-5.299439001	-3.021224306
ZNF440	-1.541264226	-3.249432558	-0.71563588	-1.037690091	-0.310712083
ZSWIM4	0.061257148	-1.216561405	0.203283647	-1.57957814	-1.382855329
ZXDC		0.153551494	-4.096463033	-1.566458073	-2.498413923
ZZEF1	-2.224053394	-1.559544395	-0.087979173	-2.164103121	-0.662993955



Appendix B IPA analysis identified embryonic development as the top biological function in which hypermethylated genes were enriched during AR and PSA induction.

Category	Functions Annotated	p-Value	Molecules	# Molecules
Embryonic Development	patterning of bone	8.43E-05	BMP7,CTNNB1,EPB41L5,HIRA,HIST1H1C,HIST1H1D,PCGF2,VCL	8
Embryonic Development	patterning of axis	4.20E-04	BMP7,CTNNB1,EPB41L5,HIRA,HIST1H1C,HIST1H1D,VCL	7
Embryonic Development	formation of anlage	6.35E-04	BMP7,CTNNB1,PAX3,WNT5A	4
Embryonic Development	abnormal morphology	8.96E-04	MEOX2,SIK3,SULF2,WNT5A	4
Embryonic Development	maintenance of embryo	1.00E-03	CTNNB1,PAX3	2
Embryonic Development	size of embryonic	1.68E-03	BTG2,CTNNB1,HIRA,MEOX2,VCL,WNT5A	6
Embryonic Development	formation of smooth	1.98E-03	MAP3K7,PTGER4	2
Embryonic Development	formation of muscle	2.41E-03	EDN1,ILK,MAP3K7,PAX3,PTGER4,VIM	6
Embryonic Development	lack of caudal vertebrae	3.26E-03	MEOX2,WNT5A	2
Embryonic Development	abnormal morphology	3.48E-03	BMP7,EDN1,PCGF2	3
Embryonic Development	morphology of dermis	4.11E-03	ARHGEF7,CTNNA2,ROCK2	3
Embryonic Development	cardiogenesis	6.38E-03	ADM,BMP7,CCND2,CTNNB1,EDN1,HIRA,MAP3K7,MED1,MIR17HG,MOSPD3,PAX3,SHC1,TMOD1,VCL,WNT5A	15
Embryonic Development	mass of kidney	7.81E-03	ADM,GHR,LRRK2,SIK3,TSC22D1	5
Embryonic Development	cell division of embryo	8.80E-03	BMP7,RGL2	2
Embryonic Development	branching of neurite	9.29E-03	ARHGEF7,BMP7,CRMP1,CTNNA2,DBN1,GRASP,NEFL,ROCK2,SULF2,WNT5A	10
Embryonic Development	dendritic growth/branching	9.67E-03	ARHGEF7,BMP7,CRMP1,CTNNA2,DBN1,GRASP,NEFL,ROCK2	8
Embryonic Development	development of somite	1.04E-02	BMP7,ENPP2,G6PD,MEOX2,PCGF2,VCL	6
Embryonic Development	abnormal morphology	1.12E-02	EGFLAM,THRB	2
Embryonic Development	development of axon	1.12E-02	MEOX2,RING1	2
Embryonic Development	development of neurite	1.23E-02	ENPP2,HIRA,HIST1H1C,HIST1H1D,PAX3,PCGF2,VCL,WNT5A	8
Embryonic Development	development of striated muscle	1.30E-02	IFRD1,MBNL1,MEOX2,PAX3,TMOD1,VCL,VIM	7
Embryonic Development	abnormal morphology	1.31E-02	BMP7,SULF2,WNT5A	3
Embryonic Development	formation of prostate	1.38E-02	BMP7,WNT5A	2
Embryonic Development	morphology of vertebral	1.62E-02	ANTXR1,MEOX2,PCGF2,RING1,SIK3,SULF2,WNT5A	7
Embryonic Development	development of muscle	1.63E-02	CTNNB1,DTNBP1,EDN1,IFRD1,ILK,MAP3K7,MBNL1,MED1,MEOX2,PAX3,SHC1,TMOD1,VCL,VIM	14
Embryonic Development	cell spreading of embryo	1.67E-02	ANTXR1,VIM	2
Embryonic Development	development of muscle	1.67E-02	TMOD1,VCL	2
Embryonic Development	morphogenesis of embryo	1.67E-02	CTNNB1,EPB41L5	2
Embryonic Development	patterning of embryo	1.74E-02	CTNNB1,MAP3K7,MEOX2	3
Embryonic Development	angiogenesis of placenta	1.84E-02	RUNX1	1
Embryonic Development	attachment of embryo	1.84E-02	ANTXR1	1
Embryonic Development	cell division of mesoderm	1.84E-02	BMP7	1

Embryonic Develo	development of hy	1.84E-02	BMP7	1
Embryonic Develo	development of pa	1.84E-02	SIM1	1
Embryonic Develo	differentiation of c	1.84E-02	TBR1	1
Embryonic Develo	differentiation of in	1.84E-02	CTNNB1	1
Embryonic Develo	differentiation of n	1.84E-02	BMP7	1
Embryonic Develo	epithelial-mesench	1.84E-02	CTNNB1	1
Embryonic Develo	formation of cardia	1.84E-02	CTNNB1	1
Embryonic Develo	formation of mam	1.84E-02	CTNNB1	1
Embryonic Develo	formation of myof	1.84E-02	VIM	1
Embryonic Develo	formation of somit	1.84E-02	PAX3	1
Embryonic Develo	induction of long b	1.84E-02	BMP7	1
Embryonic Develo	induction of metar	1.84E-02	BMP7	1
Embryonic Develo	initiation of format	1.84E-02	BMP7	1
Embryonic Develo	looping morphoge	1.84E-02	TMOD1	1
Embryonic Develo	maintenance of ap	1.84E-02	CTNNB1	1
Embryonic Develo	morphogenesis of	1.84E-02	WNT5A	1
Embryonic Develo	morphogenesis of	1.84E-02	ARHGEF7	1
Embryonic Develo	morphology of tra	1.84E-02	RYR2	1
Embryonic Develo	onset of regressio	1.84E-02	CTNNB1	1
Embryonic Develo	outgrowth of skele	1.84E-02	WNT5A	1
Embryonic Develo	patterning of meso	1.84E-02	MAP3K7	1
Embryonic Develo	patterning of vitell	1.84E-02	CTNNB1	1
Embryonic Develo	polarization of epil	1.84E-02	ILK	1
Embryonic Develo	remodeling of duc	1.84E-02	PTGER4	1
Embryonic Develo	size of ventricular	1.84E-02	CTNNB1	1
Embryonic Develo	development of le	1.90E-02	ATF4,BMP7,MED1	3
Embryonic Develo	development of ec	1.96E-02	CTNNB1,EPB41L5,KRT6B,VCL	4
Embryonic Develo	abnormal morphol	1.98E-02	ATF4,SIK3	2
Embryonic Develo	development of all	1.98E-02	BMP7,ENPP2	2
Embryonic Develo	formation of body	1.98E-02	CSNK1D,CTNNB1	2

**Appendix C Canonical pathways and upstream regulators identified by IPA using genes in Table S5.**

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Antigen Presentation Pathway	3.79E+00	1.75E-01	CALR,HLA-C,HLA-B,HLA-DRB1,PSMB8,HLA-DQA2,HLA-DRB5
nNOS Signaling in Neurons	3.13E+00	1.35E-01	GRIN2B,CALM1 (includes others),DLG2,PPP3CC,RASD1,PFKM,PRKCB
Citrulline Biosynthesis	2.77E+00	1.15E-01	GLS,ARG2,ALDH18A1
RANK Signaling in Osteoclasts	2.69E+00	9.47E-02	CALM1 (includes others),FOS,MAP3K7,PIK3C3,MAPK10,NFATC1,PPP3CC,BIRC3,XIAP
Caveolar-mediated Endocytosis Signaling	2.57E+00	9.41E-02	COPZ1,ITSN1,HLA-C,RAB5C,CAV1,HLA-B,FLOT1,ACTG1
DNA damage-induced 14-3-3 $\sigma$ Signaling	2.54E+00	1.90E-01	CCNE1,RAD17,RAD9A,RAD1
Protein Ubiquitination Pathway	2.38E+00	6.34E-02	UBE2H,DNAJC19,TCEB2,UBE2V2,CDC23,MDM2,PSMB8,XIAP,USP8,NEDD4,HLA-C,PSMD12,PSMD10,HLA-B,UBA1,USP49,BIRC3
Virus Entry via Endocytic Pathways	2.08E+00	8.08E-02	ITSN1,HLA-C,PIK3C3,CLTC,CAV1,HLA-B,ACTG1,PRKCB
Mechanisms of Viral Exit from Host Cells	2.04E+00	1.11E-01	CHMP6,NEDD4,ACTG1,CHMP3,PRKCB
Superpathway of Citrulline Metabolism	2.02E+00	7.89E-02	GLS,ARG2,ALDH18A1
Protein Kinase A Signaling	1.94E+00	5.29E-02	MYH10,SHH,CDC23,NFATC1,PYGL,PPP3CC,PLCL2,PDE4D,PLCH2,CALM1 (includes others),PTPRB,ACP1,EYA3,KDELR3,SMAD4,PDE5A,DUSP4,RYR1,CDC16,GNG4,PRKCB
Molecular Mechanisms of Cancer	1.83E+00	5.03E-02	SHH,RHOC,ARHGEF17,MDM2,XIAP,FOS,CCNE1,RHOQ,ARHGEF10,MAP3K7,PIK3C3,CDK4,MAPK10,RASGRF1,SMAD4,BMP6,BIRC3,CASP7,PRKCB
EIF2 Signaling	1.77E+00	6.00E-02	EIF2AK4,RPL15,EIF3B,RPL34,RPL39,PIK3C3,EIF3A,RPS13,EIF2B3,EIF4A2,RPL9,RPLP0
OX40 Signaling Pathway	1.69E+00	7.45E-02	TRAF3,HLA-C,MAPK10,HLA-B,HLA-DRB1,HLA-DQA2,HLA-DRB5
TWEAK Signaling	1.67E+00	1.05E-01	TRAF3,BIRC3,CASP7,XIAP
Cellular Effects of Sildenafil (Viagra)	1.64E+00	6.12E-02	CALM1 (includes others),MYH10,GUCY1A3,PDE5A,PLCL2,PLCH2,PDE4D,ACTG1,CACNA1A
Inhibition of Angiogenesis by TSP1	1.63E+00	1.03E-01	CD47,SDC1,GUCY1A3,MAPK10
Type I Diabetes Mellitus Signaling	1.61E+00	6.67E-02	HLA-C,MAP3K7,MAPK10,HLA-B,HLA-DRB1,SOC5,HLA-DRB5,IRF1
Cardiac Hypertrophy Signaling	1.54E+00	5.33E-02	CALM1 (includes others),RHOQ,MAP3K7,RHOC,PIK3C3,MAPK10,EIF2B3,ADRA2C,PLCL2,PPP3CC,PLCH2,GNG4,CACNA1A
Ephrin B Signaling	1.51E+00	7.41E-02	ITSN1,EFNB1,ACP1,CXCL12,ITSN2,GNG4
Sorbitol Degradation I	1.49E+00	2.00E-01	SORD
Nur77 Signaling in T Lymphocytes	1.49E+00	7.94E-02	CALM1 (includes others),HLA-DRB1,NFATC1,PPP3CC,HLA-DRB5
April Mediated Signaling	1.47E+00	9.30E-02	FOS,TRAF3,MAPK10,NFATC1
CD28 Signaling in T Helper Cells	1.45E+00	6.06E-02	CALM1 (includes others),FOS,PIK3C3,MAPK10,HLA-DRB1,NFATC1,PPP3CC,HLA-DRB5
Dopamine-DARPP32 Feedback in cAMP Signaling	1.44E+00	5.46E-02	GRIN2B,CALM1 (includes others),GUCY1A3,PPP2R5C,PPP3CC,PLCL2,PLCH2,DRD2,CACNA1A,PRKCB
HER-2 Signaling in Breast Cancer	1.43E+00	7.50E-02	CCNE1,PIK3C3,PARD6B,MDM2,ERBB2,PRKCB
PDGF Signaling	1.41E+00	7.06E-02	FOS,PIK3C3,ACP1,CAV1,SPHK1,PRKCB
B Cell Activating Factor Signaling	1.40E+00	8.89E-02	FOS,TRAF3,MAPK10,NFATC1
Amyotrophic Lateral Sclerosis Signaling	1.38E+00	5.93E-02	GRIN2B,PIK3C3,RAB5C,BIRC3,CASP7,XIAP,CACNA1A
Reelin Signaling in Neurons	1.36E+00	7.32E-02	ARHGEF10,MAPT,PIK3C3,HCK,MAPK10,MAP4K1
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	1.36E+00	6.74E-02	CALM1 (includes others),FOS,MAPK10,SMAD4,NFATC1,PPP3CC
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	1.34E+00	7.06E-02	HLA-C,HLA-B,HLA-DRB1,HLA-DQA2,HLA-DRB5,CASP7
Gluconeogenesis I	1.34E+00	6.12E-02	PGK1,ENO1,ME2
Glioblastoma Multiforme Signaling	1.31E+00	5.49E-02	CCNE1,RHOQ,WNT3A,RHOC,PIK3C3,CDK4,MDM2,PLCL2,PLCH2
Calcium-induced T Lymphocyte Apoptosis	1.30E+00	7.14E-02	CALM1 (includes others),HLA-DRB1,PPP3CC,HLA-DRB5,PRKCB
Glycolysis I	1.29E+00	6.98E-02	PGK1,ENO1,PFKM
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	1.29E+00	5.04E-02	CALM1 (includes others),FOS,WNT3A,MAP3K7,PIK3C3,MAPK10,SMAD4,NFATC1,PPP3CC,BMP6,BIRC3,XIAP
CD40 Signaling	1.27E+00	7.14E-02	FOS,TRAF3,MAP3K7,PIK3C3,MAPK10
PI3K Signaling in B Lymphocytes	1.24E+00	5.71E-02	CALM1 (includes others),FOS,PIK3AP1,NFATC1,PPP3CC,PLCL2,PLCH2,PRKCB
Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency	1.24E+00	8.89E-02	NANOG,NR2F2,PHC3,FBXO15
ErbB Signaling	1.24E+00	6.90E-02	FOS,BTC,PIK3C3,MAPK10,ERBB2,PRKCB

Pancreatic Adenocarcinoma Signaling	1.23E+00	5.83E-02	CCNE1,PIK3C3,CDK4,MAPK10,SMAD4,MDM2,ERBB2
TNFR2 Signaling	1.21E+00	9.09E-02	FOS,BIRC3,XIAP
Graft-versus-Host Disease Signaling	1.21E+00	8.00E-02	HLA-C,HLA-B,HLA-DRB1,HLA-DRB5
Axonal Guidance Signaling	1.19E+00	4.27E-02	SHH,ITSN1,ADAM15,CXCL12,NFATC1,PPP3CC,PLCL2,PLCH2,SEMA6C,SRGAP3,WNT3A,PIK3C3,S
Sulfate Activation for Sulfonation	1.19E+00	1.25E-01	PAPSS1
Anandamide Degradation	1.19E+00	2.00E-01	FAAH2
Glutamine Degradation I	1.19E+00	2.00E-01	GLS
Sphingosine-1-phosphate Signaling	1.19E+00	5.83E-02	RHOQ,RHOC,PIK3C3,SPHK1,PLCL2,PLCH2,CASP7
Autoimmune Thyroid Disease Signaling	1.18E+00	6.56E-02	HLA-C,HLA-B,HLA-DRB1,HLA-DRB5
TNFR1 Signaling	1.18E+00	7.69E-02	FOS,BIRC3,CASP7,XIAP
Gap Junction Signaling	1.18E+00	5.11E-02	GUCY1A3,PIK3C3,CAV1,PPP3CC,PLCL2,PLCH2,DRD2,ACTG1,PRKCB
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	1.17E+00	4.76E-02	FOS,RHOQ,MAP3K7,RHOC,PIK3C3,MAPK10,PPP2R5C,ARG2,IRF1,PRKCB
Crosstalk between Dendritic Cells and Natural Killer Cells	1.16E+00	6.32E-02	MICB,HLA-C,HLA-B,HLA-DRB1,ACTG1,HLA-DRB5
Androgen Signaling	1.16E+00	4.86E-02	CALM1 (includes others),CALR,CCNH,NCOA4,GNG4,PRKCB,POLR2K
CCR5 Signaling in Macrophages	1.14E+00	5.26E-02	CALM1 (includes others),FOS,MAPK10,GNG4,PRKCB
Cdc42 Signaling	1.11E+00	5.08E-02	FOS,HLA-C,MAPK10,HLA-B,HLA-DRB1,TNK2,HLA-DQA2,HLA-DRB5,CLIP1
PEDF Signaling	1.09E+00	6.41E-02	HNF1B,PIK3C3,ZEB1,CASP7,TCF12
nNOS Signaling in Skeletal Muscle Cells	1.08E+00	6.45E-02	CALM1 (includes others),RYR1
Dermatan Sulfate Degradation (Metazoa)	1.08E+00	8.70E-02	HYAL3,FGFRL1
PKC $\epsilon$ Signaling in T Lymphocytes	1.08E+00	4.90E-02	FOS,MAP3K7,PIK3C3,HLA-DRB1,NFATC1,PPP3CC,HLA-DRB5
BMP signaling pathway	1.07E+00	6.25E-02	MAP3K7,MAPK10,SMAD4,BMP6,XIAP
SAPK/JNK Signaling	1.07E+00	5.88E-02	MAP3K7,PIK3C3,MAPK10,MAP4K1,NFATC1,DUSP4
14-3-3-mediated Signaling	1.06E+00	5.79E-02	FOS,MAPT,PIK3C3,MAPK10,PLCL2,PLCH2,PRKCB
LPS-stimulated MAPK Signaling	1.05E+00	6.10E-02	FOS,MAP3K7,PIK3C3,MAPK10,PRKCB
Prolactin Signaling	1.05E+00	6.25E-02	FOS,PIK3C3,SOC5,IRF1,PRKCB
Mouse Embryonic Stem Cell Pluripotency	1.05E+00	6.06E-02	NANOG,WNT3A,MAP3K7,PIK3C3,SMAD4,XIAP
NADH Repair	1.03E+00	1.11E-01	CARKD
Spermidine Biosynthesis I	1.03E+00	1.25E-01	SRM
Endothelin-1 Signaling	1.00E+00	4.81E-02	FOS,GUCY1A3,PIK3C3,MAPK10,EDNRA,PLCL2,PLCH2,CASP7,PRKCB
Role of CHK Proteins in Cell Cycle Checkpoint Control	9.88E-01	7.02E-02	RAD17,RAD9A,PPP2R5C,RAD1
Cell Cycle Regulation by BTG Family Proteins	9.84E-01	8.33E-02	CCNE1,CDK4,PPP2R5C
G $\epsilon$ ±q Signaling	9.74E-01	4.76E-02	CALM1 (includes others),RHOQ,RHOC,PIK3C3,NFATC1,PPP3CC,GNG4,PRKCB
Neuropathic Pain Signaling In Dorsal Horn Neurons	9.72E-01	5.56E-02	GRIN2B,FOS,PIK3C3,PLCL2,PLCH2,PRKCB
RhoGDI Signaling	9.66E-01	4.55E-02	ARHGAP6,ARHGEF10,RHOQ,RHOC,RDX,ARHGAP12,ARHGEF17,GNG4,ACTG1
Nitric Oxide Signaling in the Cardiovascular System	9.61E-01	5.05E-02	CALM1 (includes others),GUCY1A3,PIK3C3,CAV1,CACNA1A
Glioma Invasiveness Signaling	9.45E-01	6.67E-02	RHOQ,RHOC,HMMR,PIK3C3
Cardiomyocyte Differentiation via BMP Receptors	9.42E-01	1.00E-01	MAP3K7,SMAD4
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	9.42E-01	5.56E-02	FDPS,HADHA
HIF1 $\epsilon$ ± Signaling	9.27E-01	5.56E-02	EPO,PIK3C3,TCEB2,MAPK10,MDM2,P4HTM
CXCR4 Signaling	9.25E-01	4.76E-02	FOS,RHOQ,RHOC,PIK3C3,CXCL12,MAPK10,GNG4,PRKCB
Serine Biosynthesis	9.08E-01	7.69E-02	UBAC2
Geranylgeranyldiphosphate Biosynthesis	9.08E-01	1.25E-01	FDPS
Proline Biosynthesis I	9.08E-01	7.14E-02	ALDH18A1
Arginine Degradation I (Arginase Pathway)	9.08E-01	7.69E-02	ARG2
GADD45 Signaling	9.02E-01	9.09E-02	CCNE1,CDK4
Signaling by Rho Family GTPases	8.96E-01	4.35E-02	FOS,ARHGEF10,RHOQ,RHOC,PIK3C3,MAPK10,RDX,ARHGEF17,GNG4,ACTG1,CLIP1

Allograft Rejection Signaling	8.94E-01	5.26E-02	HLA-C,HLA-B,HLA-DRB1,HLA-DQA2,HLA-DRB5
Netrin Signaling	8.79E-01	5.26E-02	NFATC1,RYR1,PPP3CC
Germ Cell-Sertoli Cell Junction Signaling	8.79E-01	4.88E-02	EPN1,AGGF1,RHOQ,MAP3K7,RHOC,PIK3C3,MAPK10,ACTG1
Role of NFAT in Cardiac Hypertrophy	8.78E-01	4.35E-02	CALM1 (includes others),MAP3K7,PIK3C3,MAPK10,PPP3CC,PLCL2,PLCH2,GNG4,PRKCB
iCOS-iCOSL Signaling in T Helper Cells	8.70E-01	4.88E-02	CALM1 (includes others),PIK3C3,HLA-DRB1,NFATC1,PPP3CC,HLA-DRB5
Cell Cycle: G1/S Checkpoint Regulation	8.67E-01	6.06E-02	CCNE1,CDK4,SMAD4,MDM2
Lipid Antigen Presentation by CD1	8.66E-01	8.70E-02	CALR,PSAP
fMLP Signaling in Neutrophils	8.56E-01	4.65E-02	CALM1 (includes others),PIK3C3,NFATC1,PPP3CC,GNG4,PRKCB
Role of PKR in Interferon Induction and Antiviral Response	8.55E-01	6.52E-02	TRAF3,MAP3K7,IRF1
Neuroprotective Role of THOP1 in Alzheimer's Disease	8.55E-01	5.56E-02	HLA-C,MAPT,HLA-B
TR/RXR Activation	8.46E-01	5.21E-02	TBL1Y,ENO1,PIK3C3,NCOA4,MDM2
Human Embryonic Stem Cell Pluripotency	8.35E-01	4.46E-02	NANOG,WNT3A,PIK3C3,SPHK1,SMAD4,FGFRL1,BMP6
Antiproliferative Role of Somatostatin Receptor 2	8.30E-01	5.63E-02	GUCY1A3,SSTR2,PIK3C3,GNG4
GM-CSF Signaling	8.30E-01	5.88E-02	PIK3C3,HCK,PPP3CC,PRKCB
CMP-N-acetylneuraminate Biosynthesis I (Eukaryotes)	8.18E-01	5.56E-02	NANP
Trans, trans-farnesyl Diphosphate Biosynthesis	8.18E-01	1.00E-01	FDPS
Factors Promoting Cardiogenesis in Vertebrates	8.17E-01	5.32E-02	CCNE1,MAP3K7,SMAD4,BMP6,PRKCB
Mitochondrial Dysfunction	8.12E-01	4.02E-02	NDUFV3,MAPK10,NDUFA12,CYC1,DHODH,NDUFA2,COX7C
Melanoma Signaling	8.10E-01	6.52E-02	PIK3C3,CDK4,MDM2
Maturity Onset Diabetes of Young (MODY) Signaling	7.99E-01	6.45E-02	HNF1B,CACNA1A
Hypoxia Signaling in the Cardiovascular System	7.96E-01	6.06E-02	EPO,UBE2H,UBE2V2,MDM2
Thrombin Signaling	7.89E-01	4.37E-02	GATA5,ARHGEF10,RHOQ,RHOC,PIK3C3,PLCL2,PLCH2,GNG4,PRKCB
mTOR Signaling	7.80E-01	4.29E-02	RHOQ,EIF3B,RHOC,PIK3C3,EIF3A,RPS13,PPP2R5C,EIF4A2,PRKCB
Aryl Hydrocarbon Receptor Signaling	7.78E-01	4.35E-02	FOS,CYP1A1,CCNE1,CDK4,SLC35A2,MDM2,ALDH18A1
iNOS Signaling	7.67E-01	5.66E-02	CALM1 (includes others),FOS,IRF1
cAMP-mediated signaling	7.63E-01	4.46E-02	CALM1 (includes others),AVPR2,PKIB,PTH1R,PDE5A,ADRA2C,DUSP4,PPP3CC,PDE4D,DRD2
Erythropoietin Signaling	7.63E-01	5.13E-02	EPO,FOS,PIK3C3,PRKCB
CTLA4 Signaling in Cytotoxic T Lymphocytes	7.47E-01	5.10E-02	PIK3C3,CLTC,HLA-DRB1,PPP2R5C,HLA-DRB5
GDNF Family Ligand-Receptor Interactions	7.47E-01	5.48E-02	FOS,PIK3C3,MAPK10,RET
Remodeling of Epithelial Adherens Junctions	7.47E-01	5.88E-02	RAB5C,MAPRE2,ACTG1,CLIP1
Huntington's Disease Signaling	7.46E-01	4.17E-02	GRIN2B,CPLX2,GLS,PIK3C3,CLTC,VT11B,GNG4,CASP7,PRKCB,POLR2K
Superpathway of Serine and Glycine Biosynthesis I	7.45E-01	5.56E-02	UBAC2
Urea Cycle	7.45E-01	5.00E-02	ARG2
Chondroitin and Dermatan Biosynthesis	7.45E-01	7.69E-02	CHSY1
Ceramide Biosynthesis	7.45E-01	6.25E-02	DEGS2
Arginine Degradation VI (Arginase 2 Pathway)	7.45E-01	6.25E-02	ARG2
Estrogen-mediated S-phase Entry	7.39E-01	7.14E-02	CCNE1,CDK4
HMGB1 Signaling	7.33E-01	5.05E-02	FOS,RHOQ,RHOC,PIK3C3,MAPK10
Growth Hormone Signaling	7.31E-01	5.26E-02	FOS,PIK3C3,SOCSS5,PRKCB
Chemokine Signaling	7.31E-01	5.48E-02	CALM1 (includes others),FOS,CXCL12,PRKCB
Role of NFAT in Regulation of the Immune Response	7.24E-01	4.04E-02	CALM1 (includes others),FOS,PIK3C3,HLA-DRB1,NFATC1,PPP3CC,GNG4,HLA-DRB5
Synaptic Long Term Potentiation	7.20E-01	4.65E-02	GRIN2B,CALM1 (includes others),PPP3CC,PLCL2,PLCH2,PRKCB
p70S6K Signaling	7.20E-01	4.65E-02	MAPT,PIK3C3,PPP2R5C,PLCL2,PLCH2,PRKCB
P2Y Purigenic Receptor Signaling Pathway	7.20E-01	4.35E-02	FOS,PIK3C3,PLCL2,PLCH2,GNG4,PRKCB

Melatonin Signaling	7.16E-01	5.13E-02	CALM1 (includes others),PLCL2,PLCH2,PRKCB
IL-17A Signaling in Gastric Cells	7.12E-01	8.00E-02	FOS,MAPK10
Glioma Signaling	7.08E-01	4.46E-02	CALM1 (includes others),PIK3C3,CDK4,MDM2,PRKCB
CREB Signaling in Neurons	7.05E-01	3.94E-02	GRIN2B,CALM1 (includes others),PIK3C3,PLCL2,PLCH2,GNG4,PRKCB,POLR2K
IL-3 Signaling	7.01E-01	5.41E-02	FOS,PIK3C3,PPP3CC,PRKCB
Small Cell Lung Cancer Signaling	7.01E-01	4.49E-02	TRAF3,CCNE1,PIK3C3,CDK4
Regulation of eIF4 and p70S6K Signaling	6.95E-01	4.02E-02	EIF3B,PIK3C3,EIF3A,RPS13,EIF2B3,PPP2R5C,EIF4A2
Antiproliferative Role of TOB in T Cell Signaling	6.86E-01	7.69E-02	CCNE1,SMAD4
Inositol Pyrophosphates Biosynthesis	6.85E-01	6.25E-02	IP6K2
T Cell Receptor Signaling	6.83E-01	4.59E-02	CALM1 (includes others),FOS,PIK3C3,NFATC1,PPP3CC
Dendritic Cell Maturation	6.70E-01	3.86E-02	HLA-C,PIK3C3,MAPK10,HLA-B,HLA-DRB1,PLCL2,PLCH2,HLA-DRB5
HGF Signaling	6.59E-01	4.76E-02	FOS,MAP3K7,PIK3C3,MAPK10,PRKCB
IL-4 Signaling	6.59E-01	5.06E-02	PIK3C3,HLA-DRB1,NFATC1,HLA-DRB5
Aldosterone Signaling in Epithelial Cells	6.48E-01	4.17E-02	NEDD4,PIK3C3,DNAJC19,PLCL2,PLCH2,SCNN1B,PRKCB
CD27 Signaling in Lymphocytes	6.39E-01	5.26E-02	FOS,MAP3K7,MAPK10
Cholecystokinin/Gastrin-mediated Signaling	6.36E-01	4.72E-02	FOS,RHOQ,RHOC,MAPK10,PRKCB
NRF2-mediated Oxidative Stress Response	6.36E-01	4.17E-02	FOS,MAP3K7,PIK3C3,DNAJC19,SLC35A2,MAFK,ACTG1,PRKCB
Semaphorin Signaling in Neurons	6.23E-01	5.77E-02	RHOQ,RHOC,DPYSL4
Superpathway of Cholesterol Biosynthesis	6.16E-01	2.33E-02	FDPS,HADHA
Cardiac $\alpha$ -adrenergic Signaling	5.97E-01	3.90E-02	PKIB,PDE5A,PPP2R5C,PDE4D,GNG4,CACNA1A
Clathrin-mediated Endocytosis Signaling	5.96E-01	4.08E-02	SH3BP4,EPN1,PIK3C3,RAB5C,CLTC,MDM2,PPP3CC,ACTG1
ILK Signaling	5.96E-01	4.17E-02	MYH10,FOS,RHOQ,RHOC,PIK3C3,MAPK10,PPP2R5C,ACTG1
B Cell Receptor Signaling	5.95E-01	4.12E-02	CALM1 (includes others),MAP3K7,PIK3C3,PIK3AP1,NFATC1,PPP3CC,PRKCB
Ceramide Signaling	5.94E-01	4.55E-02	FOS,PIK3C3,SPHK1,PPP2R5C
Cyclins and Cell Cycle Regulation	5.94E-01	4.49E-02	CCNH,CCNE1,CDK4,PPP2R5C
Assembly of RNA Polymerase I Complex	5.90E-01	7.69E-02	TAF1C
Ketolysis	5.90E-01	5.56E-02	HADHA
Thrombopoietin Signaling	5.78E-01	4.76E-02	FOS,PIK3C3,PRKCB
Relaxin Signaling	5.69E-01	3.77E-02	FOS,GUCY1A3,PIK3C3,PDE5A,PDE4D,GNG4
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	5.62E-01	3.61E-02	CALM1 (includes others),FOS,TRAF3,WNT3A,MAP3K7,PIK3C3,CXCL12,NFATC1,PPP3CC,PLCL2,PLCH2,PRKCB
B Cell Development	5.55E-01	6.06E-02	HLA-DRB1,HLA-DRB5
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	5.53E-01	4.39E-02	NANOG,WNT3A,PIK3C3,SMAD4,BMP6
G $\alpha$ s Signaling	5.53E-01	4.13E-02	AVPR2,PTH1R,HCK,RYR1,GNG4
Embryonic Stem Cell Differentiation into Cardiac Lineages	5.51E-01	1.00E-01	NANOG
NAD Phosphorylation and Dephosphorylation	5.51E-01	5.88E-02	ACP1
Glycogen Degradation II	5.51E-01	6.25E-02	PYGL
Breast Cancer Regulation by Stathmin1	5.50E-01	3.86E-02	CALM1 (includes others),CCNE1,ARHGEF10,PIK3C3,ARHGEF17,PPP2R5C,GNG4,PRKCB
Glutamate Receptor Signaling	5.49E-01	4.35E-02	GRIN2B,CALM1 (includes others),GLS
TGF- $\alpha$ Signaling	5.48E-01	4.49E-02	FOS,MAP3K7,SMAD4,MAP4K1
Leukocyte Extravasation Signaling	5.43E-01	3.98E-02	ARHGAP6,PIK3C3,CXCL12,MAPK10,RDX,ARHGAP12,ACTG1,PRKCB
Triacylglycerol Biosynthesis	5.36E-01	4.35E-02	LPPR2,ELOVL6
Death Receptor Signaling	5.36E-01	4.69E-02	BIRC3,CASP7,XIAP
Corticotropin Releasing Hormone Signaling	5.34E-01	3.68E-02	SHH,CALM1 (includes others),FOS,GUCY1A3,PRKCB
Synaptic Long Term Depression	5.27E-01	3.77E-02	GUCY1A3,RYR1,PPP2R5C,PLCL2,PLCH2,PRKCB
Induction of Apoptosis by HIV1	5.23E-01	4.62E-02	MAPK10,BIRC3,XIAP
ATM Signaling	5.23E-01	4.92E-02	MAPK10,RAD9A,MDM2
Role of JAK2 in Hormone-like Cytokine Signaling	5.19E-01	5.56E-02	EPO,SOCSS5
tRNA Splicing	5.19E-01	4.44E-02	PDE5A,PDE4D
Interferon Signaling	5.19E-01	5.56E-02	PSMB8,IRF1

Glutaryl-CoA Degradation	5.16E-01	4.17E-02	HADHA
Ketogenesis	5.16E-01	4.76E-02	HADHA
CE±-Adrenergic Signaling	5.15E-01	3.81E-02	CALM1 (includes others),PYGL,GNG4,PRKCB
IL-17A Signaling in Fibroblasts	5.02E-01	5.00E-02	FOS,MAP3K7
Nucleotide Excision Repair Pathway	5.02E-01	5.71E-02	CCNH,POLR2K
Type II Diabetes Mellitus Signaling	4.89E-01	3.11E-02	MAP3K7,PIK3C3,MAPK10,SOC5,PRKCB
Hereditary Breast Cancer Signaling	4.89E-01	3.91E-02	PIK3C3,CDK4,FANCF,FANCA,POLR2K
Cleavage and Polyadenylation of Pre-mRNA	4.85E-01	8.33E-02	CSTF2
Hematopoiesis from Multipotent Stem Cells	4.85E-01	8.33E-02	EPO
Glycogen Degradation III	4.85E-01	5.56E-02	PYGL
RhoA Signaling	4.80E-01	4.17E-02	ARHGAP6,RDX,ARHGAP12,PFN2,ACTG1
IL-17A Signaling in Airway Cells	4.74E-01	4.17E-02	MAP3K7,PIK3C3,MAPK10
Phospholipase C Signaling	4.73E-01	3.46E-02	CALM1 (includes others),ARHGEF10,RHOQ,RHOC,ARHGEF17,NFATC1,PPP3CC,GNG4,PRKCB
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	4.72E-01	3.60E-02	WBP11,PPM1H,ACP1,PALD1,NUDT15
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	4.72E-01	3.60E-02	WBP11,PPM1H,ACP1,PALD1,NUDT15
3-phosphoinositide Biosynthesis	4.72E-01	3.43E-02	WBP11,PIK3C3,PPM1H,ACP1,PALD1,NUDT15
Communication between Innate and Adaptive Immune Cells	4.66E-01	3.67E-02	HLA-C,HLA-B,HLA-DRB1,HLA-DRB5
IL-1 Signaling	4.66E-01	3.74E-02	FOS,MAP3K7,MAPK10,GNG4
VEGF Signaling	4.66E-01	3.88E-02	PIK3C3,EIF2B3,ACTG1,PRKCB
Sertoli Cell-Sertoli Cell Junction Signaling	4.60E-01	3.59E-02	MPP6,EPN1,AGGF1,GUCY1A3,MAP3K7,MAPK10,ACTG1
Assembly of RNA Polymerase III Complex	4.57E-01	6.25E-02	BRF1
Non-Small Cell Lung Cancer Signaling	4.51E-01	3.80E-02	PIK3C3,CDK4,ERBB2
Calcium Signaling	4.47E-01	3.32E-02	GRIN2B,CALM1 (includes others),MYH10,CALR,NFATC1,RYR1,PPP3CC
Chronic Myeloid Leukemia Signaling	4.38E-01	3.81E-02	PIK3C3,CDK4,SMAD4,MDM2
Chondroitin Sulfate Degradation (Metazoa)	4.32E-01	4.35E-02	HYAL3
Mevalonate Pathway I	4.32E-01	3.57E-02	HADHA
Mitotic Roles of Polo-Like Kinase	4.30E-01	4.29E-02	PPP2R5C,CDC23,CDC16
JAK/Stat Signaling	4.30E-01	4.29E-02	FOS,PIK3C3,SOC5
Neurotrophin/TRK Signaling	4.30E-01	4.00E-02	FOS,SPRY2,PIK3C3
Tight Junction Signaling	4.22E-01	3.73E-02	MYH10,FOS,CDK4,CSTF2,PPP2R5C,ACTG1
IL-10 Signaling	4.20E-01	3.85E-02	FOS,MAP3K7,ARG2
Agrin Interactions at Neuromuscular Junction	4.20E-01	4.35E-02	MAPK10,ERBB2,ACTG1
Superpathway of Inositol Phosphate Compounds	4.16E-01	3.08E-02	WBP11,PIK3C3,PPM1H,ACP1,PALD1,IP6K2,NUDT15
MIF Regulation of Innate Immunity	4.13E-01	4.00E-02	FOS,MAPK10
FcεRIIB Signaling in B Lymphocytes	4.13E-01	3.39E-02	PIK3C3,MAPK10
IGF-1 Signaling	4.12E-01	3.81E-02	FOS,NEDD4,PIK3C3,SOC5
IL-8 Signaling	4.10E-01	3.41E-02	FOS,RHOQ,RHOC,PIK3C3,MAPK10,GNG4,PRKCB
Telomere Extension by Telomerase	4.08E-01	5.88E-02	TINF2
Isoleucine Degradation I	4.08E-01	3.33E-02	HADHA
Methionine Degradation I (to Homocysteine)	4.08E-01	4.35E-02	PRMT8
Renal Cell Carcinoma Signaling	4.00E-01	4.05E-02	FOS,PIK3C3,TCEB2
Basal Cell Carcinoma Signaling	4.00E-01	4.11E-02	SHH,WNT3A,BMP6
IL-17 Signaling	3.81E-01	4.05E-02	MAP3K7,PIK3C3,MAPK10
Systemic Lupus Erythematosus Signaling	3.74E-01	3.24E-02	SNRNP35,FOS,HLA-C,PIK3C3,PRPF39,HLA-B,NFATC1,LSM4
AMPK Signaling	3.69E-01	2.99E-02	PIK3C3,ADRA2C,PPP2R5C,PFKFB2,PFKM
Cysteine Biosynthesis III (mammalia)	3.67E-01	3.33E-02	PRMT8
MSP-RON Signaling Pathway	3.65E-01	4.00E-02	PIK3C3,ACTG1

Leptin Signaling in Obesity	3.64E-01	3.61E-02	PIK3C3,PLCL2,PLCH2
IL-12 Signaling and Production in Macrophages	3.56E-01	3.21E-02	FOS,PIK3C3,MAPK10,IRF1,PRKCB
D-myo-inositol-5-phosphate Metabolism	3.56E-01	3.21E-02	WBP11,PPM1H,ACP1,PALD1,NUDT15
3-phosphoinositide Degradation	3.50E-01	3.18E-02	WBP11,PPM1H,ACP1,PALD1,NUDT15
G-Protein Coupled Receptor Signaling	3.49E-01	3.31E-02	AVPR2,PIK3C3,PTH1R,PDE5A,ADRA2C,DUSP4,PDE4D,DRD2,PRKCB
Valine Degradation I	3.49E-01	2.86E-02	HADHA
Endoplasmic Reticulum Stress Pathway	3.49E-01	5.56E-02	CASP7
VEGF Family Ligand-Receptor Interactions	3.47E-01	3.57E-02	FOS,PIK3C3,PRKCB
Granzyme A Signaling	3.32E-01	5.00E-02	HMGB2
Renin-Angiotensin Signaling	3.31E-01	3.20E-02	FOS,PIK3C3,MAPK10,PRKCB
Glucocorticoid Receptor Signaling	3.23E-01	3.06E-02	FOS,CCNH,MAP3K7,PIK3C3,MAPK10,SMAD4,NFATC1,PPP3CC,POLR2K
Tryptophan Degradation III (Eukaryotic)	3.16E-01	2.08E-02	HADHA
Assembly of RNA Polymerase II Complex	3.13E-01	3.57E-02	CCNH,POLR2K
RAR Activation	3.07E-01	3.17E-02	FOS,CCNH,NR2F2,MAPK10,SMAD4,PRKCB
Ephrin Receptor Signaling	3.07E-01	2.99E-02	GRIN2B,ITSN1,EFNB1,ACP1,CXCL12,GNG4
Regulation of Actin-based Motility by Rho	3.01E-01	3.37E-02	RHOQ,RHOC,PFN2
Prostate Cancer Signaling	3.01E-01	3.06E-02	CCNE1,PIK3C3,MDM2
Endometrial Cancer Signaling	2.95E-01	3.51E-02	PIK3C3,ERBB2
CCR3 Signaling in Eosinophils	2.93E-01	3.15E-02	CALM1 (includes others),PIK3C3,GNG4,PRKCB
Epithelial Adherens Junction Signaling	2.93E-01	3.40E-02	MYH10,EPN1,AGGF1,ACTG1,CLIP1
Colorectal Cancer Metastasis Signaling	2.92E-01	3.10E-02	FOS,RHOQ,WNT3A,RHOC,PIK3C3,MAPK10,SMAD4,GNG4
Polyamine Regulation in Colon Cancer	2.87E-01	3.45E-02	PSME3
NAD Salvage Pathway II	2.87E-01	3.23E-02	ACP1
Pyrimidine Ribonucleotides Interconversion	2.87E-01	2.94E-02	CTPS2
IL-2 Signaling	2.86E-01	3.45E-02	FOS,PIK3C3
IL-6 Signaling	2.82E-01	3.23E-02	FOS,MAP3K7,PIK3C3,MAPK10
Lymphotoxin $\alpha$ Receptor Signaling	2.78E-01	3.28E-02	TRAF3,PIK3C3
Role of IL-17A in Arthritis	2.78E-01	3.17E-02	PIK3C3,MAPK10
FAK Signaling	2.74E-01	2.97E-02	HMMR,PIK3C3,ACTG1
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	2.74E-01	3.26E-02	TRAF3,HLA-DRB1,HLA-DRB5
CDK5 Signaling	2.67E-01	3.19E-02	MAPT,PPP2R5C,CACNA1A
Actin Nucleation by ARP-WASP Complex	2.62E-01	3.03E-02	RHOQ,RHOC
Phospholipases	2.62E-01	3.03E-02	PLCL2,PLCH2
Regulation of Cellular Mechanics by Calpain Protease	2.62E-01	2.78E-02	CCNE1,CDK4
Toll-like Receptor Signaling	2.62E-01	3.23E-02	FOS,MAP3K7
EGF Signaling	2.62E-01	3.23E-02	FOS,PIK3C3
IL-22 Signaling	2.62E-01	4.00E-02	MAPK10
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	2.62E-01	3.70E-02	FDPS
Tumoricidal Function of Hepatic Natural Killer Cells	2.62E-01	4.17E-02	CASP7
Pyrimidine Ribonucleotides De Novo Biosynthesis	2.62E-01	2.08E-02	CTPS2
Neuregulin Signaling	2.61E-01	2.94E-02	BTC,ERBB2,PRKCB
Bladder Cancer Signaling	2.61E-01	3.30E-02	CDK4,MDM2,ERBB2
G Beta Gamma Signaling	2.61E-01	2.56E-02	CAV1,GNG4,PRKCB
Apoptosis Signaling	2.61E-01	3.16E-02	BIRC3,CASP7,XIAP
GCE $\alpha$ 1 Signaling	2.60E-01	3.03E-02	CAV1,ADRA2C,DRD2,GNG4
ErbB2-ErbB3 Signaling	2.54E-01	3.33E-02	PIK3C3,ERBB2



Role of JAK family kinases in IL-6-type Cytokine Signaling	2.50E-01	3.70E-02	MAPK10
Myc Mediated Apoptosis Signaling	2.47E-01	3.33E-02	PIK3C3,MAPK10
Bupropion Degradation	2.39E-01	3.03E-02	CYP1A1
Role of BRCA1 in DNA Damage Response	2.33E-01	3.08E-02	FANCF,FANCA
ErbB4 Signaling	2.33E-01	2.99E-02	PIK3C3,PRKCB
IL-15 Production	2.29E-01	3.23E-02	IRF1
Cell Cycle Control of Chromosomal Replication	2.29E-01	3.23E-02	CDK4
Acetone Degradation I (to Methylglyoxal)	2.29E-01	2.78E-02	CYP1A1
Sonic Hedgehog Signaling	2.10E-01	3.03E-02	SHH
Fatty Acid $\beta$ -oxidation I Superpathway of	2.01E-01	2.22E-02	HADHA
Methionine Degradation	2.01E-01	1.56E-02	PRMT8